Hits	Search Text	DBs	Time Stamp
469	two adj hybrid	USPAT; EPO; JPO; Derwent	2000/10/31 12:22
9558	protein adj protein	USPAT; EPO; JPO; Derwent	2000/10/31 12:24
927	interaction and (protein adj protein)	USPAT; EPO; JPO; Derwent	2000/10/31 12:25
257	(protein adj protein) adj interaction	USPAT; EPO; JPO; Derwent	2000/10/31 16:16
14	(two adj hybrid) and ((protein adj protein) adj interaction)	USPAT; EPO; JPO; Derwent	2000/10/31 12:43
4	(green adj fluorescent adj protein) and ((two adj hybrid) and ((protein adj protein) adj interaction))	USPAT; EPO; JPO; Derwent	2000/10/31 12:45
2	(mutant or mutated or defective) adj 125	USPAT; EPO; JPO; Derwent	2000/10/31 15:26
85	green adj fluorescent adj protein	USPAT; EPO; JPO; Derwent	2000/10/31 15:26
18	short-jay.in. or short-jay-m.in.	USPAT; EPO; JPO; Derwent	2000/10/31 16:26
	(protein adj protein) adj interaction and 137	USPAT; EPO; JPO; Derwent	2000/10/31 16:22

10/31/00
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Attach paper #8

C 9/529,458
STN/CAS
Attachment #8

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TERMINAL ENTER 1, 2, 3, OR ? :2

FILE 'HOME' ENTERED AT 17:20:22 ON 31 OCT 2000

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FULL ESTIMATED COST	0.90	1.05

FILE 'BIOSIS' ENTERED AT 17:21:56 ON 31 OCT 2000
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CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 25 October 2000 (20001025/ED)

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for details.

=> two hybrid

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        1230081 TWO
             46 TWOS
        1230111 TWO
                (TWO OR TWOS)
          5[illegible]47 HYBRID
          35361 HYBRIDS
          82474 HYBRID
                (HYBRID OR HYBRIDS)
L2         3903 TWO HYBRID
                (TWO(W)HYBRID)
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=> [illegible] protein interaction?

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[illegible]
[illegible]
[illegible]
                (PROTEIN OR PROTEINS
[illegible] PROTEIN
          [illegible]45 PROTEINS
[illegible]
                (PROTEIN OR PROTEINS)
[illegible]
[illegible]
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[illegible] 2
1807528 3

L5 [illegible] 2 AND 3

=> dup rem l5

L6 [illegible] L5 AND L4

=> dup rem l6

MISSING OPERATOR L2 SAME
The search profile that was entered contains terms or
quoted terms that are not separated by a logical operator.

=> modulator or effector or dissassociator

7729 MODULATOR
5835 MODULATORS
12928 MODULATOR
(MODULATOR OR MODULATORS)
24500 EFFECTOR
7032 EFFECTORS
30162 EFFECTOR
(EFFECTOR OR EFFECTORS)
0 DISSASSOCIATOR
L7 42849 MODULATOR OR EFFECTOR OR DISSASSOCIATOR

=> l6 and l7

L8 21 L6 AND L7

=> d ibib abs tot

L8 ANSWER 1 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 2000:439021 BIOSIS
DOCUMENT NUMBER: PREV200000439021
TITLE: The junctional multidomain protein AF-6 is a binding partner of the Rap1A GTPase and associates with the actin cytoskeletal regulator profilin.
AUTHOR(S): Boettner, Benjamin; Govek, Eve-Ellen; Cross, Justin; Van Aelst, Linda (1)
CORPORATE SOURCE: (1) Cold Spring Harbor Laboratories, 1 Bungtown Road, Cold Spring Harbor, NY, 11724 USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (August 1, 2000) Vol. 97, No. 16, pp. 9064-9069. print.
[illegible]
[illegible]
[illegible]
[illegible]
AB The AF-6 protein is a multidomain protein that contains two putative Ras-binding domains within its N terminus. Because of this feature, AF-6 has been isolated in both ***two*** - ***hybrid*** and biochemical [illegible] and is postulated to be a potential Ras- ***effector*** protein. Herein, we show that it is specifically the first Ras-binding [illegible] AF-6 that mediates this interaction and that the Ras-related Rap1A protein can associate with this motif [illegible] with similar affinity to that of H-, K-, and N-Ras. We further demonstrate that AF-6 has

L8 ANSWER 2 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 2000:242206 BIOSIS
DOCUMENT NUMBER: PREV200000242206
TITLE: Retinoic acid and its receptors repress the expression and transactivation functions of Nur77: A possible mechanism for the inhibition of apoptosis by retinoic acid.
AUTHOR(S): Pang, Hyo-Jin; Song, Mi-Ryoung; Lee, Soo-Kyung; Shin, Pul-Chul; Choi, Youn-Hee; Kim, Se Jong; Lee, Jae Woon; Lee, Mi-Ock [1]
CORPORATE SOURCE: [1] Department of Microbiology, Institute for Immunology and Immunological Diseases, Yonsei University College of Medicine, Seoul, 120-752 South Korea
SOURCE: Experimental Cell Research, (May 1, 2000) Vol. 256, No. 2, pp. 545-554.
ISSN: 0014-4827.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Nur77 (NGFI-B) is an orphan nuclear receptor that has been implicated in activation-induced T-cell apoptosis. Retinoids, potent immune ***modulators*** , were shown to inhibit the activation-induced apoptosis of immature thymocytes and T-cell hybridomas. To illustrate the mechanism of the inhibition, we examined the effects of retinoic acid (RA) on the expression and transactivation functions of Nur77 in the human peripheral blood mononuclear cells and the human T-cell leukemia, Jurkat. All-trans-RA remarkably repressed the DNA binding and transcriptional induction of Nur77. Among the two potential trans-acting factors that activate Nur77 gene promoter, i.e., AP-1 and related serum response factor (RSRF), all-trans-RA repressed DNA binding and reporter gene activity of AP-1 but not that of RSRF, suggesting that the inhibition may be mediated through AP-1. We also demonstrated a posttranscriptional regulation of Nur77 function by retinoid receptors by showing that transactivation activity of Nur77 was significantly inhibited by cotransfection of RARalpha or RXRalpha. Nur77 bound RARalpha or RXRalpha in both yeast and mammalian ***two*** - ***hybrid*** tests, suggesting that direct ***protein*** - ***protein*** ***interaction*** between these receptors may mediate the inhibition. Taken all together, we demonstrated that RA repressed Nur77 function through multiple mechanisms that may provide the basis for RA inhibition on the apoptosis of activated T-lymphocytes.

L8 ANSWER 3 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1998:496666 BIOSIS
DOCUMENT NUMBER: PREV199800496666
TITLE: The Borgs, a new family of Cdc42 and TC10 GTPase-interacting proteins.
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: [illegible]
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB [illegible]

HA-tagged Borg3 protein was mostly cytosolic when expressed [illegible] in NIH 3T3 cells, with some accumulation in membrane ruffles. The phenotype induced by Borg3 was reminiscent of that caused by an inhibition of Rho function and was reversed by overexpression of Rho. Surprisingly, it was independent of the ability to bind Cdc42. Borg3 also inhibited [illegible] kinase activity by a mechanism that was independent of Cdc42 binding. HA-Borg3 expression caused substantial delays in the spreading of cells on [illegible] surfaces after replating, and the spread cells lacked stress fibers. We propose that the Borg proteins function as negative regulators of Rho GTPase signaling.

L4 ANSWER 4 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1999:488133 BIOSIS
DOCUMENT NUMBER: PREV199900488133

TITLE: Two distinct mutations of the RET receptor causing Hirschsprung's disease impair the binding of signalling ***effectors*** to a multifunctional docking site.

AUTHOR(S): Geneste, Olivier; Bidaud, Christelle; De Vita, Gabriella; Hofstra, Robert M. W.; Tartare-Deckert, Sophie; Buys, Charles H. C. M.; Lenoir, Gilbert M.; Santoro, Massimo; Billaud, Marc (1)
CORPORATE SOURCE: (1) Laboratoire de Genetique, CNRS UMR5641, 8 avenue Rockefeller, 69373, Lyon Cedex 08 France

SOURCE: Human Molecular Genetics, (Oct., 1999) Vol. 8, No. 11, pp. 1989-1999.
ISSN: 0964-6906.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The RET gene codes for a transmembrane tyrosine kinase which is a subunit of a multimeric complex that acts as a receptor for four structurally related molecules: the glial cell line-derived neurotrophic factor (GDNF), neurturin, artemin and persephin. Germline mutations of RET cause a dominantly inherited dysgenesis of the enteric nervous system known as Hirschsprung's disease (HSCR; aganglionosis megacolon). The majority of HSCR mutations results either in a reduction of dosage of the RET protein or in the loss of RET function. Two novel distinct mutations of RET that led either to the deletion of codon 1059 (denoted DELTA1059) or to the substitution of a Pro for Leu1061 have been identified in five HSCR families. In one large pedigree, two children born from asymptomatic consanguineous parents presented a severe form of HSCR and were found to carry the mutation at codon 1061 in the homozygous state. A tyrosine residue at position 1062 is an intracytoplasmic docking site that enables RET to recruit several signalling molecules, including the Shc adaptor protein. We now report that both HSCR mutations impair the fixation of Shc to RET and consequently prevent its phosphorylation. In addition, quantitative analysis in PC12 cells reveals that mutation DELTA1059 [illegible] biochemical explanation for the phenotype of patients carrying a homozygous mutation at codon 1061. Finally, these data indicate that Y1062 is a multifunctional docking site that confers to RET the capacity to [illegible] downstream signalling pathways which exert a crucial role during [illegible].

LANGUAGE: English
SUMMARY LANGUAGE: English

AB Fibroblast growth factors (FGF) activate their receptors through the formation of trimolecular complexes, composed of a ligand, a receptor, and a heparan sulfate oligosaccharide, all of which are members of particularly large families capable of multiple interactions in a combinatorial fashion. Understanding this large network of interactions not only presents a great challenge, but is practically beyond the capacity of most classical techniques routinely used to study ligand receptor interactions. We have used the yeast ***two*** ***hybrid*** system to study ***protein*** - ***protein*** ***interactions*** in the FGF family. Both ligand and receptor ectodomains are properly folded and functional in the yeast. Basic FGF (bFGF) expressed in the yeast dimerizes spontaneously. This self-assembly occurs at low affinity, which can be greatly enhanced by the introduction of heparin, supporting a defined role for heparin in bFGF dimerization. Screening a rat embryo cDNA library with bFGF in the yeast ***two*** ***hybrid*** system identified a short variant of FGF receptor 1, found most frequently in embryonal and tumor cells and which possesses affinity toward bFGF that is significantly greater than that of the more abundant, full-length receptor. We find the yeast ***two*** ***hybrid*** system, a most suitable alternative method for the analysis of growth factor-receptor interactions as well as for screening for novel interacting proteins and ***modulators*** of FGF and its receptors.

L6 ANSWER 6 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1999:255910 BIOSIS
DOCUMENT NUMBER: PREV199900255910
TITLE: The ubiquitin-homology protein, DAP-1, associates with tumor necrosis factor receptor (p60) death domain and induces apoptosis.
AUTHOR(S): Liou, Mei-Ling; Liou, Hsiou-Chi (1)
CORPORATE SOURCE: (1) Division of Immunology, Department of Medicine, Graduate School of Medical Sciences, Cornell University Medical College, New York, NY, 10021 USA
SOURCE: Journal of Biological Chemistry, (April 9, 1999) Vol. 274, No. 15, pp. 10145-10153.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The tumor necrosis factor receptor, p60 (TNF-R1), transduces death signals via the association of its cytoplasmic domain with several intracellular proteins. By screening a mammalian cDNA library using the yeast ***two*** - ***hybrid*** cloning technique, we isolated a ubiquitin-homology protein, DAP-1, which specifically interacts with the cytoplasmic death domain of TNF-R1. Sequence analysis reveals that DAP-1 shares striking sequence homology with the yeast SMT3 protein that is [illegible] (Meluh, P. B., and Koshland, D. [illegible] Mol. Biol. Cell [illegible]). DAP-1 [illegible] with the [illegible] [illegible] Boddy, M. N., Howe, K., [illegible], and Freemont, P. S. [illegible], and the sentrin protein, which associates with the Fas death receptor (Okura, T., Gong, L., Kamitani, T., Wada, T., Okura, I., Wei, C. F., Chang, H. M., and Yeh, E. T. (1996) J. Immunol. 157, 4277-4281). The in vivo interaction between DAP-1 and TNF-R1 was further confirmed in mammalian cells. In transient transfection assays, overexpression of DAP-1 [illegible] NF-kappaB [illegible] activity in [illegible] cells, a human kidney embryonic [illegible]

domain [illegible] transcription factor.
AUTHOR: Daniel, [illegible] M.; Reynolds, Albert B. [illegible]
CORP. AUTHOR SOURCE: [illegible] Department of Cell Biology, Vanderbilt University, 1161 21st Ave. South, Nashville, TN, 37232-2175 USA
SOURCE: Molecular and Cellular Biology, May, 1999 Vol. 19, No. 5, pp. 3614-3623.
ISSN: 0270-7306.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB p120ctn is an Armadillo repeat domain protein with structural similarity to the cell adhesion cofactors beta-catenin and plakoglobin. All three proteins interact directly with the cytoplasmic domain of the transmembrane cell adhesion molecule E-cadherin; beta-catenin and plakoglobin bind a carboxy-terminal region in a mutually exclusive manner, while p120 binds the juxtamembrane region. Unlike beta-catenin and plakoglobin, p120 does not interact with alpha-catenin, the tumor suppressor adenomatous polyposis coli (APC), or the transcription factor Lef-1, suggesting that it has unique binding partners and plays a distinct role in the cadherin-catenin complex. Using p120 as bait, we conducted a yeast ***two*** - ***hybrid*** screen and identified a novel transcription factor which we named Kaiso. Kaiso's deduced amino acid sequence revealed an amino-terminal BTB/POZ ***protein*** - ***protein*** ***interaction*** domain and three carboxy-terminal zinc fingers of the C2H2 DNA-binding type. Kaiso thus belongs to a rapidly growing family of POZ-ZF transcription factors that include the Drosophila developmental regulators Tramtrak and Bric a brac, and the human oncoproteins BCL-6 and PLZF, which are causally linked to non-Hodgkins' lymphoma and acute promyelocytic leukemia, respectively. Monoclonal antibodies to Kaiso were generated and used to immunolocalize the protein and confirm the specificity of the p120-Kaiso interaction in mammalian cells. Kaiso specifically coprecipitated with a variety of p120-specific monoclonal antibodies but not with antibodies to alpha- or beta-catenin, E-cadherin, or APC. Like other POZ-ZF proteins, Kaiso localized to the nucleus and was associated with specific nuclear dots. Yeast ***two*** - ***hybrid*** interaction assays mapped the binding domains to Arm repeats 1 to 7 of p120 and the carboxy-terminal 200 amino acids of Kaiso. In addition, Kaiso homodimerized via its POZ domain but it did not heterodimerize with BCL-6, which heterodimerizes with PLZF. The involvement of POZ-ZF proteins in development and cancer makes Kaiso an interesting candidate for a downstream ***effector*** of cadherin and/or p120 signaling.

L2 ANSWER 8 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1999:247872 BIOSIS
DOCUMENT NUMBER: PREV199900247872
TITLE: Genes for calcineurin B-like proteins in Arabidopsis are differentially regulated by stress signals.
AUTHOR(S): [illegible]
CORP. AUTHOR SOURCE: [illegible]
SOURCE: [illegible]
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB [illegible]

[redacted] by a family of [redacted] six genes in Arabidopsis. [redacted] for three of these genes [redacted] this study. AtCBL1 mRNA was preferentially expressed in stems and roots and its mRNA levels strongly increased in response to specific stress signals such as drought, cold, and wounding. In contrast, AtCBL2 and AtCBL3 are constitutively expressed under all conditions investigated. Our data suggest that AtCBL1 may act as a regulatory subunit of a plant Ca2+/calmodulin-like activity mediating calcium signaling under certain stress conditions.

L4 ANSWER 9 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: [illegible] BIOSIS
DOCUMENT NUMBER: [illegible]
TITLE: Characterization of two subunits of Arabidopsis 19S proteasome regulatory complex and its possible interaction with the COP9 complex.
AUTHOR(S): Kwok, Shing F.; Staub, Jeffrey M.; Deng, Xing-Wang (1)
CORPORATE SOURCE: (1) Dep. Mol. Cell. Dev. Biol., Yale Univ., New Haven, CT 06520-8104 USA
SOURCE: Journal of Molecular Biology, (Jan. 8, 1999) Vol. 285, No. 1, pp. 85-95.
ISSN: 0022-2836.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The nuclear localized, multi-subunit COP9 complex (or COP9 signalosome) is a key developmental ***modulator*** involved in repression of photomorphogenesis. In an effort to further define the molecular actions of the COP9 complex, a yeast ***two*** ***hybrid*** interactive screen was undertaken to identify proteins that could directly interact with one subunit of this complex, namely FUS6/COP11. This screen identified one specific interactive protein, AtS9, that is likely the Arabidopsis non-ATPase S9 (subunit 9) of the 19S regulatory complex from the 26S proteasome. AtS9 specifically interacts with FUS6/COP11 via the C-terminal domain of FUS6/COP11, which is distinct from the N-terminal domain necessary for FUS6/COP11 to interact with itself. As anticipated, AtS9 is not a member of the COP9 complex, but tightly associates with an ATPase subunit of the Arabidopsis 19S proteasome regulatory complex, AtS6A. Since all three proteins, FUS6/COP11, AtS9, and AtS6A, are present as complexed forms in vivo, the observed interaction implies that the COP9 complex may directly interact with the 19S regulatory complex of the 26S proteasome or other potential AtS9-containing complex. This notion is consistent with the parallel tissue-specific expression patterns and the similar, predominantly nuclear localization of both the COP9 complex and the AtS9 protein.

L4 ANSWER 10 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1999:17905 BIOSIS
DOCUMENT NUMBER: PREV199900017905
TITLE: Gene activation by the AraC protein can be inhibited by DNA looping between AraC and a DNA sequence that interacts with AraC's [illegible] ***two*** - ***hybrid*** system.
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible] USA
SOURCE: Molecular Microbiology, (Nov., 1998) Vol. 30, No. 3, pp. 615-624.
ISSN: [illegible]
DOCUMENT TYPE: Article
LANGUAGE: English

...s, we have utilized the properties of this protein to study the ***effector*** protein to achieve a new mode of gene regulation by DNA looping, in which the activator protein is an essential part of the repressor complex. The flexibility of the DNA loop may facilitate this novel combinatorial arrangement of these proteins on the DNA. The requirement for protein interactions between the AraC and LexA hybrids in gene regulation suggests that this regulatory circuit may prove useful as an E. coli-based ***two*** - ***hybrid*** system.

L8 ANSWER 11 OF 21 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:446728 BIOSIS
DOCUMENT NUMBER: PREV199800446728
TITLE: Small protein domains direct dimerization and homotypic interactions of the ***protein*** - ***protein*** ***interaction*** domain of PKR, the interferon-induced protein kinase.
AUTHOR(S): Tan, Seng-Lai; Katze, Michael G. (1)
CORPORATE SOURCE: (1) Dep. Microbiol., Sch. Med., Box 357242, Univ. Washington, Seattle, WA 98195 USA
SOURCE: Methods (Orlando), (July, 1998) Vol. 15, No. 3, pp. 207-223.
ISSN: 1046-2023.
DOCUMENT TYPE: General Review
LANGUAGE: English
AB The interferon-induced protein kinase, PKR, is a pivotal component of interferon (IFN)-induced cellular antiviral and antiproliferative response. The identification and characterization of proteins, of both viral and cellular origins, that interact with PKR have proven to be a valuable probe for unraveling the cellular regulation and function of PKR. Several studies have demonstrated that PKR forms dimers and that dimerization is likely to be required for activation and/or catalytic function. It is therefore important to elucidate the mechanism of PKR dimer formation and the role of PKR ***effectors*** in modulating kinase dimerization. Herein we describe the use of the two genetic approaches, the lambda repressor fusion and the yeast ***two*** - ***hybrid*** systems, to detect and analyze homo- and heterotypic interactions with PKR. We also describe several biochemical methodologies commonly used in our laboratory to validate the genetic results. Although the examples in this article focus on PKR, the techniques can easily be adapted to investigate protein-protein associations in a variety of experimental systems. Finally, given the important role of PKR as a mediator of IFN-induced antiviral and antiproliferative effects, these studies may provide clues to the development of reagents that target PKR to enhance the therapeutic use of IFN in the treatment of disease.

L8 ANSWER 12 OF 21 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 1998:236123 BIOSIS
DOCUMENT NUMBER: PREV199800236123
TITLE: [illegible]
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: [illegible]

system and in an in vitro [illegible] assay. Northern blot analysis revealed the major transcript [illegible] that was present in all rat tissues investigated. Rat SGT cDNA coded for 314 amino acids, and the protein migrated in sodium dodecyl sulfate-polyacrylamide gel electrophoresis with an apparent molecular mass of [illegible] kDa. SGT could be detected in both the nucleus and the cytoplasm of rat cells, as determined by indirect immunofluorescence analysis and Western blotting of fractionated cellular extracts with an affinity-purified antiserum raised against recombinant SGT (ACI.I). In H-1 virus-infected rat and human cells, compared to mock-infected controls, differences in the migration of SGT polypeptides were revealed after Western blot analysis of total cellular extracts. Moreover, the transient expression of NS proteins was sufficient to induce SGT modification. These results show that cellular SGT, which we have identified as an NS1-interacting protein, is modified by parvovirus infection as well as NS expression.

L8 ANSWER 13 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

ACCESSION NUMBER: 1998:222407 BIOSIS

DOCUMENT NUMBER: PREV199800222407

TITLE: Identification of the binding partners for flightless I, a novel protein bridging the leucine-rich repeat and the gelsolin superfamilies.

AUTHOR(S): Liu, Yu-Tsueng; Yin, Helen L. (1)

CORPORATE SOURCE: (1) Dep. Physiol., Univ. Texas Southwestern Med. Cent., Dallas, TX 75235 USA

SOURCE: Journal of Biological Chemistry, (April 3, 1998) Vol. 273, No. 14, pp. 7920-7927.
ISSN: 0021-9258.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Flightless-I (fliI) is a novel member of the gelsolin family that is important for actin organization during Drosophila embryogenesis and myogenesis. Drosophila fliI and the human homolog FLI both contain the classic gelsolin 6-fold segmental repeats and an amino-terminal extension of 16 tandem leucine-rich repeats (LRR). LRR repeats form amphipathic beta-a structural units that mediate ***protein*** - ***protein*** ***interactions*** . Although there are close to 100 known LRR domain-containing proteins, only a few binding pairs have been identified. In this paper, we used biochemical and genetic approaches to identify proteins that interact with human FLI. In vitro synthesized FLI bound to actin-Sepharose and binding was reduced by competition with excess soluble actin. Actin binding was mediated through the gelsolin-like domain and not the LRR domain. Although the FLI LRR module is most closely related to the LRR domains of Ras-interactive proteins, FLI does not associate with Ras, selected Ras ***effectors*** , or other Ras-related small GTPases. ***Two*** - ***hybrid*** screens using FLI LRR as bait identified a novel LRR binding partner. The 0.65-kilobase pair (kb) clone from the [illegible] ***two*** - ***hybrid*** [illegible] assays, [illegible] with FLI LRR. [illegible] FLAP [illegible] analyses revealed that FLAP messages [illegible] 5.1 kb, which are differentially expressed in the tissues tested. Skeletal and cardiac muscles are particularly rich in the 3.3-kb FLAP message, and the FLI message as well. Full-length FLAP clones were isolated from a mouse skeletal muscle cDNA library. They have an open reading frame which [illegible] analyses [illegible] that the FLAP protein is rich in alpha-[illegible] [illegible]

SOURCE: USA
Biology of Reproduction, Feb., 199- Vol. [illegible] No. [illegible], pp. 302-311.
ISSN: [illegible].
DOCUMENT TYPE: Article
LANGUAGE: English.
AB ***hyb*** - ***protein*** ***interact*** are essential to cellular mechanisms at all levels in biologically responsive systems. These interactions occur extracellularly and include ligand-receptor interactions, cell adhesion, antigen recognition, and virus-host recognition. Intracellular ***protein*** - ***protein*** ***interactions*** occur in the formation of multi-protein complexes, during the assembly of cytoskeletal elements, and between receptor-***effector*** , as well as ***effector*** - ***effector*** , molecules of signal transduction pathways. Finally, assembly of transcriptional machinery involves protein interactions. The yeast ***two*** - ***hybrid*** method is a powerful technique for analyzing these ***protein*** - ***protein*** ***interactions*** . Since the publication of this technique in the late 1980s, the robust nature and far-reaching utility of yeast ***two*** - ***hybrid*** systems for functional expression library cloning has led to the identification of many novel proteins in all areas of biological life science research. Additionally, ***two*** - ***hybrid*** techniques provide a rapid and versatile system for the further characterization of discrete ***protein*** - ***protein*** ***interactions*** . Recent variations on the basic system have enabled application well beyond protein pairs, to investigate multi-protein complexes and protein-nucleotide interactions. Yeast ***two*** - ***hybrid*** methods necessitate expression and subsequent interaction between a "protein of interest" functional pair within the yeast cell, ultimately driving reporter gene expression and thus effectively linking ***protein*** - ***protein*** ***interaction*** (s) to a change in yeast cell phenotype. Functional ***protein*** - ***protein*** ***interactions*** using the ***two*** - ***hybrid*** techniques have been demonstrated for all levels of cellular biology; however, until recently, extracellular ***protein*** - ***protein*** ***interactions*** were excluded from investigations using this technique. Investigations from several labs have now demonstrated that extracellular proteins can be studied using ***two*** - ***hybrid*** methods, thereby enabling intense study of extracellular protein partners using the robust nature and the genetic power of yeast.

L8 ANSWER 15 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1998:71512 BIOSIS
DOCUMENT NUMBER: PREV199[illegible]71512
TITLE: Syntenin, a PDZ protein that binds syndecan cytoplasmic domains.
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: [illegible]
pp. [illegible]-[illegible].
ISSN: [illegible].
DOCUMENT TYPE: Article
LANGUAGE: English
AB [illegible]

...signaling systems to cytoskeletal proteins in yeast through interactions with ***effectors***.

L8 ANSWER 16 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1998:[illegible] BIOSIS
DOCUMENT NUMBER: PREV[illegible]
TITLE: Discrimination of amino acids mediating ras binding from noninteracting residues affecting Raf activation by double mutant analysis.
AUTHORS: Jaitner, Birgit K.; Becker, Joerg; Linnemann, Thomas; Herrmann, Christian; Wittinghofer, Alfred; Block, Christoph [1]
CORPORATE SOURCE: [1] Postfach [illegible], D-4600 Dortmund Germany
SOURCE: Journal of Biological Chemistry, Nov. 21, 1997 Vol. [illegible], No. 47, pp. [illegible]. ISSN: [illegible].
DOCUMENT TYPE: Article
LANGUAGE: English
AB The contribution of residues outside the Ras binding domain of Raf (RafRBD) to Ras-Raf interaction and Ras-dependent Raf activation has remained unresolved. Here, we utilize a double mutant approach to identify complementary interacting amino acids that are involved in Ras-Raf interaction and activation. Biochemical analysis demonstrates that Raf-Arg59 and Raf-Arg67 from RafRBD are interacting residues complementary to Ras-Glu37 located in the Ras ***effector*** region. Raf-Arg59 and Raf-Arg67 also mediate interaction with Ras-Glu37 in Ras-dependent Raf activation. The characteristics observed here can be used as criteria for a role of residues from other regions of Raf in Ras-Raf interaction and activation. We developed a quantitative ***two*** - ***hybrid*** system as a tool to investigate the effect of point mutations on ***protein*** - ***protein*** ***interactions*** that elude biochemical analysis of bacterially expressed proteins. This assay shows that Raf-Ser257 in the RafCR2 domain does not contribute to Ras-Raf interaction and that the Raf-S257L mutation does not restore Raf binding to Ras-E37G. Yet, Raf-S257L displays high constitutive kinase activity and further activation by Ras-G12V/E37G is still impaired as compared with activation by Ras-G12V. This strongly suggests that the RafCR2 domain is an independent domain involved in the control of Raf activity and a common mechanism for constitutively activating mutants may be the interference with the inactive ground state of the kinase.

L8 ANSWER 17 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1997:514190 BIOSIS
DOCUMENT NUMBER: PREV[illegible]
TITLE: ***Modulator*** protein RsbR regulates environmental signalling in the general stress pathway of Bacillus [illegible].
AUTHORS: Akbar, Sabina; Kang, [illegible]; Schmidt, Barbara S.; Price, Chester W. [1]
CORPORATE SOURCE: [1] Dept. [illegible], Univ. [illegible], Davis, CA [illegible] USA
SOURCE: [illegible], Vol. [illegible], No. [illegible]. ISSN: [illegible].
DOCUMENT TYPE: Article
LANGUAGE: English
AB Bacillus subtilis responds to signals of environmental and nutritional stress by inducing [illegible] general stress [illegible] under the control of the [illegible]

activity in expression of sigma-E-dependent reporter fusions, RseB is likely and in combination with other rse mutations. To determine the possible interaction of RseB with other Rse proteins, we tested the ability of wild-type and mutant RseB to activate transcription in the yeast ...yw ... - ...hybrid... system in combination with other Rse regulators. On the basis of this genetic analysis, we believe that RseB is a positive regulator which modulates sigma-E activity in response to salt and heat stress. Our data further suggest that: (1) RseB interacts with an inhibitor function of RseA by direct ...protein... - ...protein... ...interaction... ; and (2) this interaction with RseA is likely controlled by the phosphorylation state of RseB.

L... ANSWER 1... OF 1... BIOSIS COPYRIGHT ... BIOSIS
ACCESSION NUMBER: 1...:...43... BIOSIS
DOCUMENT NUMBER: PREV1...98...2142
TITLE: Modulation of the Escherichia coli sigma-E (RpoE) heat-shock transcription-factor activity by the RseA, RseB and RseC proteins.
AUTHOR(S): Missiakas, Dominique; Mayer, Matthias P.; Lemaire, Marc; Georgopoulos, Costa; Raina, Satish (1)
CORPORATE SOURCE: (1) Dep. Biochimie Med., Centre Med. Univ., 1 rue Michel-Servet, 1211 Geneve 4 Switzerland
SOURCE: Molecular Microbiology, (1997) Vol. 24, No. 2, pp. 355-371. ISSN: 0950-382X.
DOCUMENT TYPE: Article
LANGUAGE: English

AB The sigma-E (RpoE) transcription factor of Escherichia coli regulates the expression of genes whose products are devoted to extracytoplasmic activities. The sigma-E regulon is induced upon misfolding of proteins in the periplasm or the outer membrane. Similar to other alternative sigma factors, the activity of sigma-E is tightly regulated in E. coli. We have previously shown that sigma-E is positively autoregulated at the transcriptional level. DNA sequencing, coupled with transcriptional analyses, have shown that sigma-E is encoded by the first gene of a four-gene operon. The second gene of this operon, rseA, encodes an anti-sigma-E activity. This was demonstrated at both the genetic and biochemical levels. For example, mutations in rseA constitutively increase sigma-E activity. Consistent with this overproduction of RseA leads to an inhibitory effect on sigma-E activity. Topological analysis of RseA suggests the existence of one transmembrane domain, with the N-terminal part localized in the cytoplasm. Overproduction of this N-terminal domain alone was shown to inhibit sigma-E activity. These observations were confirmed in vitro, because either purified RseA or only its purified N-terminal domain inhibited transcription from E-sigma-E-dependent promoters. Furthermore, RseA and sigma-E co-purify, and can be co-immunoprecipitated, and chemically cross-linked. The sigma-E activity is further modulated by the products of the remaining genes in this ...rseB, rseC and rseD. RseB is a periplasmic protein, which probably ...modulates sigma-E activity by interacting with the N-terminal ...periplasmic domain of RseA. In contrast, RseC is an inner membrane protein ...that positively affects sigma-E activity. ...RseA, RseB and RseC were purified to ...homogeneity. ...hybrid... system.

L... ANSWER 2... OF 2... BIOSIS COPYRIGHT ... BIOSIS
ACCESSION NUMBER: 1...:...414... BIOSIS
DOCUMENT NUMBER: PREV1...
TITLE: ...

[illegible] IGF-1) type 1 receptor (IGF-1R) has been reported in some studies. Interaction of SYP and GAP with IR and IGF-1R was re-investigated here in the ***two*** - ***hybrid*** system by screening bio3/lacZ activation in S. cerevisiae. The experiments were performed with the cytoplasmic beta domain of IR and IGF-1R and various SH2-subdomains of SYP and GAP. None of the subdomains of SYP and GAP tested were able to activate his3/lacZ, whereas these reporter genes were strongly activated when p85 was used as we have recently shown. Thus, interaction of SYP and GAP with IR and IGF-1R, if any, would be weak and/or transient as compared to that of p85.

L* ANSWER [illegible] OF 21 BIOSIS COPYRIGHT [illegible] BIOSIS
ACCESSION NUMBER: 1995:576173 BIOSIS
DOCUMENT NUMBER: PREV199548074476
TITLE: Interaction of the protein nucleobindin with G-alpha-i2, as revealed by the yeast ***two*** - ***hybrid*** system.
AUTHOR(S): Mochizuki, Naoki; Hibi, Masahiko; Kanai, Yoshiyuki; Insel, Paul A. (1)
CORPORATE SOURCE: (1) Dep. Pharmacol., Univ. California San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0636 USA
SOURCE: FEBS Letters, (1995) Vol. 373, No. 2, pp. 155-158. ISSN: 0014-5793.
DOCUMENT TYPE: Article
LANGUAGE: English
AB The heterotrimeric G protein, G-alpha-i2, transduces signals from seven membrane spanning receptors to ***effectors*** such as adenylyl cyclase and ion channels. The purpose of this study was to identify these or other cellular proteins that interact with G-alpha-i2 by use of the yeast ***two*** - ***hybrid*** system. A human B cell cDNA library was screened by this system using full length G-alpha-i2. Four positive colonies were obtained. Two of the four were identified as nucleobindin, a calcium binding protein and a putative antigen to which anti-nuclear antibodies are generated in mice with a disorder that resembles systemic lupus erythematosus. Nucleobindin has a leucine zipper, EF hands, and a signal peptide sequence and is thought to localize to the nucleus as well as being secreted. The specificity of interaction between G-alpha-i2 and nucleobindin was confirmed by an in vitro binding assay using recombinant proteins. Transfection of G-alpha-i2 and nucleobindin in COS cells increased G-alpha-i2 expression relative to cells transfected with G-alpha-i2 and mock vector. Our results indicate that the yeast ***two*** - ***hybrid*** system provides a means to identify novel proteins that interact with G-alpha proteins. Nucleobindin appears to represent one of those proteins.

L* ANSWER 21 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1995:76839 BIOSIS
DOCUMENT NUMBER: PREV199548004[illegible]
TITLE: [illegible]
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: [illegible]

in tyrosine phosphorylation of p62 and was mediated by both the SH3 and
SH2 domains of p59-fyn. The phosphorylation of p62 by p59-fyn required an
intact SH3 domain, demonstrating that one function of the src family
kinase SH3 domains is to bind and present certain substrates to the
kinase. As p62 contains at least five SH3-domain-binding motifs and
multiple tyrosine phosphorylation sites, p62 may interact with other
signalling molecules via SH3 and SH2 domain interactions. Here we show
that the SH3 and/or SH2 domains of the signalling proteins Grb2 and
phospholipase C-gamma-1 can interact with p62 both in vitro and in vivo.
Thus, we propose that one function of the tandemly occurring SH3 and SH2
domains of src family kinases is to bind p62, a multifunctional SH3 and
SH2 domain adapter protein, linking src family kinases to downstream
effector and regulatory molecules.

=> log h

* * * * * * RECONNECTED TO STN INTERNATIONAL * * * * * *
SESSION RESUMED IN FILE 'BIOSIS' AT 17:30:42 ON 31 OCT 2000
FILE 'BIOSIS' ENTERED AT 17:30:42 ON 31 OCT 2000
COPYRIGHT (C) 2000 BIOSIS (R)

	SINCE FILE ENTRY	TOTAL SESSION
COST IN U.S. DOLLARS	42.00	43.05

FULL ESTIMATED COST

=> d his

FILE 'BIOSIS' ENTERED AT 17:21:56 ON 31 OCT 2000
L2 3903 TWO HYBRID
L3 7748 PROTEIN PROTEIN INTERACTION?
L4 0 L2 NEAR 3
L5 1129870 L2 AND 3
L6 687 L2 AND L3
L7 42843 MODULATOR OR EFFECTOR OR DISSASSOCIATOR
L8 21 L6 AND L7

=> file biosis

	SINCE FILE ENTRY	TOTAL SESSION
COST IN U.S. DOLLARS	42.70	43.75

FULL ESTIMATED COST

FILE 'BIOSIS' ENTERED AT 17:31:11 ON 31 OCT 2000
COPYRIGHT (C) 2000 BIOSIS (R)

FILE COVERS 1969 TO DATE.
THE BIOSIS THESAURUS WAS LAST MODIFIED ON 19 JUNE 2000.
NEW CHEMICAL TERMS 1969 TO DATE.

RECORDS LAST ADDED: 25 October 2000 (20001025/ED)

THE BIOSIS THESAURUS HAS BEEN EXPANDED. ENTER HELP BIOSIS AND HELP REINDEXING
FOR DETAILS.

=> d kwic 1-4

L10 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2000 BIOSIS
TI Tyrosine sulfation: A ***modulator*** of extracellular ***protein***
- ***protein*** ***interactions*** .
ACCESSION NUMBER: 2000:226020 BIOSIS
DOCUMENT NUMBER: PREV200000226020
TITLE: Tyrosine sulfation: A ***modulator*** of extracellular
protein - ***protein*** ***interactions*** .
AUTHOR(S): Kehoe, John W.; Bertozzi, Carolyn R. (1)
CORPORATE SOURCE: (1) Department of Molecular and Cell Biology, University of
California, Berkeley, CA, 94720 USA
SOURCE: Chemistry & Biology (London), (March, 2000) Vol. 7, No. 3,
pp. R57-R61.
ISSN: 1074-5521.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L10 ANSWER 2 OF 4 BIOSIS COPYRIGHT 2000 BIOSIS
AB . . . the ras signaling pathway, i.e., it downregulates activated ras via
its catalytic domain, and it also participates in the downstream
effector signaling pathway by mediating ***protein*** -
protein ***interaction*** . Missense mutations presumably
[illegible] ras activation were previously [illegible] in this gene, in a
subset of [illegible]. Address: . .
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: [illegible]
TITLE: Expression of the [illegible]
[illegible].
AUTHOR(S): Parsons, John; Williams, John; Lowell, Ben; Burns, Alan;
Gilby, Sharon; Kay [illegible]; Sullivan, Anne; Bishop,
Ethan (1)
CORPORATE SOURCE: (1) Cancer Inst. of [illegible], Inst. Res., Chair
[illegible], [illegible]
SOURCE: [illegible], (1984) [illegible], No. [illegible].

[redacted]
AUTHOR(S):
CORPORATE SOURCE:
SOURCE:
FILE SEGMENT:
LANGUAGE:

AN [redacted]
AB. . . Ward and More is hydrophilic [redacted], and regions [redacted]
[redacted] This may should also be considered as potential [redacted]
[redacted] ***interaction*** - ***protein***
interaction sites [redacted] hydrophilic, but also
contain residues that could interact through the hydrophobic effect.
ACCESSION NUMBER: 1986:92387 BIOSIS
DOCUMENT NUMBER: BA81:2503
TITLE: ANALYSIS OF COMPUTER-GENERATED HYDROPATHY PROFILES FOR HUMAN GLYCOPROTEIN AND LACTOGENIC HORMONES.
AUTHOR(S): KRYSTEK S R JR; REICHERT L E JR; ANDERSEN T T
CORPORATE SOURCE: DEP. BIOCHEMISTRY, ALBANY MED. COLLEGE, ALBANY, NEW YORK 12208.
SOURCE: ENDOCRINOLOGY, (1985) 116 (5), 1117-1124.
CODEN: ENDOAO. ISSN: 0013-7227.
FILE SEGMENT: BA; OLD
LANGUAGE: English

=> l7(s)l3

L11 104 L7(S)L3

=> d his

FILE 'BIOSIS' ENTERED AT 17:21:56 ON 31 OCT 2000
L2 3903 TWO HYBRID
L3 7748 PROTEIN PROTEIN INTERACTION?
L4 0 2 NEAR 3
L5 1129870 2 AND 3
L6 687 L2 AND L3
L7 42849 MODULATOR OR EFFECTOR OR DISSASSOCIATOR
L8 21 L6 AND L7

FILE 'BIOSIS' ENTERED AT 17:31:11 ON 31 OCT 2000
L9 0 L7(W)L5
L10 4 L7 (5W) L5
L11 [redacted]

[redacted]

[redacted]

L11 ANSWER 1 OF 4 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . NHE-1 is an [redacted] receptor that has been implicated in [redacted]
[redacted] ***protein*** , were shown [redacted]

AUTHOR(S): Kang, Hyo-Jin; Song, Mi-Ryoung; Lee, Soo-Kyung; Shin, Eui-Chul; Choi, Youn-Hee; Kim, Se Jong; Lee, Jae Woon; Lee, Mi-Ock (1)

CORPORATE SOURCE: (1) Department of Microbiology, Institute for Immunology and Immunological Diseases, Yonsei University College of Medicine, Seoul, 120-752 South Korea

SOURCE: Experimental Cell Research, May 1, 2000 Vol. 256, No. 2, pp. 545-554.
ISSN: 0014-4827.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L17 ANSWER 1 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS

AB Nur77 (NGFI-B) is an orphan nuclear receptor that has been implicated in activation-induced T-cell apoptosis. Retinoids, potent immune ***modulators*** , were shown to inhibit the activation-induced apoptosis of immature thymocytes and T-cell hybridomas. To illustrate the mechanism of the inhibition,. . . Nur77 was significantly inhibited by cotransfection of RARalpha or RXRalpha. Nur77 bound RARalpha or RXRalpha in both yeast and mammalian ***two*** - ***hybrid*** tests, suggesting that direct ***protein*** - ***protein*** ***interaction*** between these receptors may mediate the inhibition. Taken all together, we demonstrated that RA repressed Nur77 function through multiple mechanisms. . .

ACCESSION NUMBER: 2000:242208 BIOSIS

DOCUMENT NUMBER: PREV200000242208

TITLE: Retinoic acid and its receptors repress the expression and transactivation functions of Nur77: A possible mechanism for the inhibition of apoptosis by retinoic acid.

protein-protein interaction.
ACCESSION NUMBER: 1999:[illegible] BIOSIS
DOCUMENT NUMBER: PREV199900481930
TITLE: Re-examination of fibroblast growth factor receptor interactions in the yeast ***two*** ***hybrid*** system.
AUTHOR(S): Al Ali-Brinstein, Hadi; Seitin, Andrew; Mayen, Artur (1)
CORPORATE SOURCE: (1) Department of Molecular Cell Biology, Weizmann Institute of Science, Rehovot, 76100 Israel.
SOURCE: Molecular Biotechnology, (June, 1999) Vol. 11, No. 3, pp. [illegible].
ISSN: [illegible].
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L1 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . . unique binding partners and plays a distinct role in the cadherin-catenin complex. Using p120 as bait, we conducted a yeast ***two*** - ***hybrid*** screen and identified a novel transcription factor which we named Kaiso. Kaiso's deduced amino acid sequence revealed an amino-terminal BTB/POZ ***protein*** - ***protein*** ***interaction*** domain and three carboxy-terminal zinc fingers of the C2H2 DNA-binding type. Kaiso thus belongs to a rapidly growing family of. . . E cadherin, or APC. Like other POZ-ZF proteins, Kaiso localized to the nucleus and was associated with specific nuclear dots. Yeast ***two*** - ***hybrid*** interaction assays mapped the binding domains to Arm repeats 1 to 7 of p120 and the carboxy-terminal 200 amino acids. . . . heterodimerizes with PLZF. The involvement of POZ-ZF proteins in development and cancer makes Kaiso an interesting candidate for a downstream ***effector*** of cadherin and/or p120 signaling.
ACCESSION NUMBER: 1999:248790 BIOSIS
DOCUMENT NUMBER: PREV199900248790
TITLE: The catenin p120ctn interacts with Kaiso, a novel BTB/POZ domain zinc finger transcription factor.
AUTHOR(S): Daniel, Juliet M.; Reynolds, Albert B. (1)
CORPORATE SOURCE: (1) Department of Cell Biology, Vanderbilt University, 1161 21st Ave. South, Nashville, TN, 37232-2175 USA
SOURCE: Molecular and Cellular Biology, (May, 1999) Vol. 19, No. 5, pp. 3614-3623.
ISSN: 0270-7306.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English

L1 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . . repeats and an amino-terminal extension of 16 tandem leucine-rich [illegible]. LRR repeats form amphipathic beta-a structural units that [illegible] ***two*** - ***hybrid*** [illegible]. [illegible] has-related small GTPases. ***Two*** - ***hybrid*** screens with Rit LRR as bait identified a novel LRR binding partner. The 1.4-kilobase pair (kb) clone from the screen survived additional rounds of stringent ***two*** - ***hybrid*** pairwise assays, establishing a specific [illegible] Rit LRR was [illegible] with Rit LRR. The translated protein [illegible]

TI Yeast ***two***-***hybrid*** : So many interactions, (in) so little time.

AB ***Protein*** - ***protein*** ***interactions*** are essential to cellular mechanisms at all levels in biologically responsive systems. These interactions occur extracellularly and include ligand-receptor interactions, cell adhesion, antigen recognition, and virus-host recognition. Intracellular ***protein*** - ***protein*** ***interactions*** occur in the formation of multi-protein complexes, during the assembly of cytoskeletal elements, and between receptor-***effector*** , as well as ***effector*** - ***effector*** , molecules of signal transduction pathways. Finally, assembly of transcriptional machinery involves protein interactions. The yeast ***two*** - ***hybrid*** method is a powerful technique for analyzing these ***protein*** - ***protein*** ***interactions*** . Since the publication of this technique in the late 1980s, the robust nature and far-reaching utility of yeast ***two*** - ***hybrid*** systems for functional expression library cloning has led to the identification of many novel proteins in all areas of biological life science research. Additionally, ***two*** - ***hybrid*** techniques provide a rapid and versatile system for the further characterization of discrete ***protein*** - ***protein*** ***interactions*** . Recent variations on the basic system have enabled application well beyond protein pairs, to investigate multi-protein complexes and protein-nucleotide interactions. Yeast ***two*** - ***hybrid*** methods necessitate expression and subsequent interaction between a "protein of interest" functional pair within the yeast cell, ultimately driving reporter gene expression and thus effectively linking ***protein*** - ***protein*** ***interaction*** (s) to a change in yeast cell phenotype. Functional ***protein*** - ***protein*** ***interactions*** using the ***two*** - ***hybrid*** techniques have been demonstrated for all levels of cellular biology; however, until recently, extracellular ***protein*** - ***protein*** ***interactions*** were excluded from investigations using this technique. Investigations from several labs have now demonstrated that extracellular proteins can be studied using ***two*** - ***hybrid*** methods, thereby enabling intense study of extracellular protein partners using the robust nature and the genetic power of yeast.

IT Methods & Equipment
expression library cloning: cloning method; yeast ***two*** - ***hybrid*** method: analytical method

IT Miscellaneous Descriptors
antigen recognition; cell adhesion; ligand-receptor interactions; protein-nucleotide interactions; protein-protein interactions; signal transduction; virus-host recognition

ACCESSION NUMBER: 1998:115653 BIOSIS
DOCUMENT NUMBER: PREV199800115653
TITLE: Yeast ***two*** - ***hybrid*** : So many interactions, (in) so little time.
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: Biology of Reproduction, [illegible], 58 (2), 1998, 302-311.
ISSN: 0006-3363.
DOCUMENT TYPE: Article
LANGUAGE: English

noninteracting residues affecting Ras activation by double mutant analysis.

AUTHORS: Gaither, Karin K.; Bunker, Joan; Linnemann, Thomas; Herrmann, Christian; Wittinghofer, Alfred; Block, Christ[illegible]

[illegible] Postfach [illegible], [illegible] Germany

JOURNAL: Journal of Biological Chemistry, Nov. 21, [illegible], No. 47, pp. [illegible].

ISSN: [illegible]

DOCUMENT TYPE: Article

LANGUAGE: English

> expression librar?

```
        521675 EXPRESSION
          8185 EXPRESSIONS
        526617 EXPRESSION
                 (EXPRESSION OR EXPRESSIONS)
         35894 LIBRAR?
L13       2253 EXPRESSION LIBRAR?
                 (EXPRESSION(W)LIBRAR?)
```

> l1 and l13

```
L14         21 L2 AND L13
```

> d kwic tot

L14 ANSWER 1 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

AB. . . involves interactions between extracellular matrix proteins. To identify proteins interacting with tuftelin, a potential nucleator of enamel crystallites, the yeast ***two*** - ***hybrid*** system was applied to a mouse tooth ***expression*** ***library*** and a tuftelin-interacting protein (TIP) was isolated for further characterization. Polyclonal antibodies were prepared against two recombinant variants of this. . .

L14 ANSWER 2 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

AB. . . specific association with other proteins. To discover proteins that associate with hsp27, we made a differentiated rat Sertoli cell cDNA ***expression*** ***library*** and screened it using the yeast ***two*** - ***hybrid*** system. We obtained a cDNA coding for a novel protein of 428 amino acids that we have named PASS1 (protein. . .

L14 ANSWER 3 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS

AB. . . [illegible] ***expression*** ***library*** [illegible] ***two*** - ***hybrid*** [illegible] Schizosaccharomyces pombe. The cDNA was [illegible] an Schizosaccharomyces pombe ***expression*** ***library*** by a ***two*** - ***hybrid*** selection for clones encoding calmodulin (CaM)-binding proteins. The predicted protein is highly homologous to mammalian [illegible], including a CaM-binding [illegible]. . .

[redacted] amino acid residues. We further. . .

IT Methods & Equipment
yeast ***two*** - ***hybrid*** screen: screening method

IT Miscellaneous descriptors
calcium-dependent cellular process; signaling pathway

L14 ANSWER [redacted] OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB . . . [redacted] AB N-terminal peptide as a probe to screen the human testis
expression ***library*** , we identified an ARA [redacted]
AB N-terminal-[redacted] protein ARALY8, which consists of 1, 21 amino
acids with an apparent molecular mass of. . . The far-Western blotting
and co-immunoprecipitation assays demonstrate that the AB can interact
directly with ARALY8/RMP. Affinity gel pull-down and mammalian ***two***
- ***hybrid*** assays further suggest another two proteins
similarly the interaction between AB and ARALY8. Transient
transfection assays demonstrated that ARALY8 might. . .

IT . . .
co-immunoprecipitation: analytical method, precipitation techniques;
reporter gene assay: genetic analysis, genetic method; transient
transfection assay: Recombinant DNA Technology, genetic method;
two - ***hybrid*** assay: genetic analysis, genetic method;
S-protein affinity gel pull-down assay: activity assays, analytical
method; Western blot: detection method, gene mapping,. . .

L14 ANSWER 6 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
TI Identification of a rice APETALA3 homologue by yeast ***two*** -
hybrid screening.
AB A cDNA clone OsMADS16 was isolated from the rice young inflorescence cDNA
expression ***library*** by the yeast ***two*** -
hybrid screening method with OsMADS4 as bait. We have previously
shown that the OsMADS4 gene is a member of the PI. . . expression
patternsof the OsMADS16 and OsMADS4 genes are very similar to those of AP3
and PI, respectively. In the yeast ***two*** - ***hybrid*** system,
OsMADS4 interacted only with OsMADS16 among several rice MADS genes
investigated, suggesting that OsMADS4 and OsMADS16 function as a. . .
IT Sequence Data
AF077760: DDBJ, EMBL, GenBank, amino acid sequence, nucleotide sequence
IT Methods & Equipment
two - ***hybrid*** screening: screening method

L14 ANSWER [redacted] OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB The yeast ***two*** - ***hybrid*** system has been used to identify
mammalian clones that interact with poliovirus 2A proteinase (2Apro).
Eight clones which encode previously unidentified human proteins were
[redacted] ***expression*** ***library*** . In
[redacted]
. .

[redacted]
TI A cloning method for caspase substrates that uses the yeast ***two*** -
hybrid system: Cloning of the antiapoptotic gene baculovirus.
AB. . . of caspases. We established a method for cloning the genes of
caspase substrates by two major modifications of the yeast ***two*** -
hybrid system: [redacted]
. .

two - ***hybrid*** system.

AB . . . a novel gene/protein family. Since [illegible]-like protein [illegible] are all predicted to contain a coiled-coil domain, we used the yeast ***two*** - ***hybrid*** system and glutathione S-transferase pull-down assays to investigate whether homo- and/or heteromeric interactions occur between [illegible]-like proteins. Analyses of yeast. . . [illegible]-like proteins interact in homo- and heteromeric fashions through their predicted coiled-coil domains. Similarly, extensive ***two*** ***hybrid*** screenings of a human breast carcinoma ***expression*** ***library*** identified [illegible] as potential interactors for both [illegible] and [illegible]. Thus, [illegible]-like proteins appear to exert and/or. . .

L14 ANSWER 1? OF ?1 BIOSIS COPYRIGHT 2000 BIOSIS

AB A 16-mer peptide library was screened using the yeast ***two*** - ***hybrid*** system to identify peptides which specifically interact with the human papillomavirus type 16 (HPV-16) E6 protein. Four different peptides were. . . an EL-LN-G motif. A fifth E6 binding peptide, derived from the putative tumour suppressor protein tuberin, was identified during a ***two*** - ***hybrid*** screen of a HeLa cDNA ***expression*** ***library*** . This peptide contained a D-I-L-G motif. Homology to the peptides was found within the E6 binding proteins E6AP and E6-BP.. . .

L14 ANSWER 11 OF ?1 BIOSIS COPYRIGHT 2000 BIOSIS

TI Yeast ***two*** - ***hybrid*** : So many interactions, (in) so little time.

AB . . . receptor-effector, as well as effector-effector, molecules of signal transduction pathways. Finally, assembly of transcriptional machinery involves protein interactions. The yeast ***two*** - ***hybrid*** method is a powerful technique for analyzing these protein-protein interactions. Since the publication of this technique in the late 1980s, the robust nature and far-reaching utility of yeast ***two*** - ***hybrid*** systems for functional ***expression*** ***library*** cloning has led to the identification of many novel proteins in all areas of biological life science research. Additionally, ***two*** - ***hybrid*** techniques provide a rapid and versatile system for the further characterization of discrete protein-protein interactions. Recent variations on the basic system have enabled application well beyond protein pairs, to investigate multi-protein complexes and protein-nucleotide interactions. Yeast ***two*** - ***hybrid*** methods necessitate expression and subsequent interaction between a "protein of interest" functional pair within the yeast cell, ultimately driving reporter. . . gene expression and thus effectively linking protein-protein interaction(s) to a change in yeast cell phenotype. Functional protein-protein interactions using the ***two*** - ***hybrid*** techniques have been demonstrated for all levels of cellular biology; however, until recently, extracellular protein-protein [illegible] ***two*** - ***hybrid*** [illegible]

IT Methods & Equipment
expression ***library*** cloning: cloning method; yeast ***two*** - ***hybrid*** method: analytical method

IT Miscellaneous Descriptors
[illegible]; cell adhesion; [illegible] interactions; [illegible] interactions; [illegible]-protein interactions; [illegible]

AB. . . that interact with [redacted]. A proline-rich region of [redacted] an SH3-binding domain was used to screen an embryo cDNA [redacted] ***expression*** ***library***, and a cDNA clone was isolated and shown to be alpha-actinin. A yeast ***two*** - ***hybrid*** analysis showed a specific interaction between the proline-rich region of SpStx and a putative SH3 domain of the sea urchin. . .

L14 ANSWER 14 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB A ***two*** - ***hybrid*** system was used to screen yeast and human ***expression*** ***libraries*** for proteins that interact with mismatch repair proteins. PCNA was recovered from both libraries and was in the case of. . .

L14 ANSWER 15 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . via the Box and B-box motifs, we attempted to isolate proteins interacting with HBP-1a(17) based on protein-protein interactions. A cDNA ***expression*** ***library*** from which candidates was screened with full-length HBP-1a(17), and a bZIP-type protein, termed HALF-1 (HBP-1-associated leucine-zipper factor-1), was isolated. GST-pulldown assay, yeast ***two*** - ***hybrid*** system and EMSA showed that HALF-1 and HBP1a(17) interact with each other through their leucine-zipper regions. Dissection experiments showed that. . .

L14 ANSWER 16 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . possibility that it has multiple roles in the viral life cycle. To obtain possible insights into these roles, the yeast ***two*** - ***hybrid*** system was used to examine the interactions of the 52/55-kDa protein with viral and cellular factors. cDNA ***expression*** ***libraries*** from human 293 cells at both early and late stages of adenovirus type 5 infection were constructed and screened, with. . . was shown to interact with a bacterial glutathione S-transferase-52/55-kDa fusion protein in vitro, further supporting the finding with the yeast ***two*** - ***hybrid*** system. Finally, coimmunoprecipitation studies confirmed that the 52/55-kDa protein and IVa2 polypeptide interact specifically during the course of adenovirus infection.. . .

L14 ANSWER 17 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
AB A HeLa cDNA ***expression*** ***library*** was screened for human polypeptides that interacted with the poliovirus RNA-dependent RNA polymerase, 3D, using the ***two*** - ***hybrid*** system in the yeast Saccharomyces cerevisiae. Sam68 (Src-associated in mitosis, 68 kDa) emerged as the human cDNA that, when fused. . .

L14 ANSWER 18 OF 21 BIOSIS COPYRIGHT 2000 BIOSIS
IT Miscellaneous Descriptors
ENZYMES; GENE CLONING; HUMAN MYOTONIC DYSTROPHY; MEETING ABSTRACT; MEETING POSTER; MOUSE CARDIAC COMPLEMENTARY DNA ***EXPRESSION*** ***LIBRARY*** ; PATH 1CC2; PLASMID; SIGNAL TRANSDUCTION PATHWAYS; ***TWO*** - ***HYBRID*** SYSTEM

[redacted]

AB. . . CDK2 and cyclins C, D, and E. The recent development of strategies, such as the one-hybrid and ***two*** - ***hybrid*** systems, has broadened the repertoire of roles that can be [redacted] ***expression*** ***libraries*** is [redacted]

[illegible] ANSWER [illegible] PLOS [illegible] PRINT [illegible] PLOS

AB [illegible] of most lipoproteins and plays an important role in their
metabolism. Recently, apoB cDNA clones have been isolated from an
expression ***library*** made with mRNA from a human hepatoma
line. These clones, which were [illegible] bases long and
[illegible] to a [illegible] sequence, were used in [illegible]
situ hybridization studies, [illegible] were demonstrated with mRNAs re-
[illegible], ***rat*** ***hybrid*** with [illegible]
transcripts that [illegible] the [illegible] are [illegible] with the pre-[illegible]
A third hybrid with [illegible]

tsien/au

FILE 'BIOSIS' ENTERED AT 17:31:16 ON 31 OCT 2001

L2 3403 TWO HYBRID
L3 7748 PROTEIN PROTEIN INTERACTION?
L4 0 2 NEAR 3
L5 1124870 2 AND 3
L6 [illegible] L2 AND L3
L7 42943 MODULATOR OR EFFECTOR OR DISSOCIATOR
L8 21 L6 AND L7

FILE 'BIOSIS' ENTERED AT 17:31:11 ON 31 OCT 2001
L9 0 L7 (W) L3
L10 4 L7 (5W) L3
L11 104 L7(S)L3
L12 6 L2 AND L11
L13 2253 EXPRESSION LIBRAR?
L14 21 L2 AND L13
L15 0 TSIEN/AU
L16 1 TANDEM FLUORESCENT PROTEIN

=> (tsien r? or tsien, r?)/au,in

584 TSIEN R?/AU
9 TSIEN R?/IN
584 TSIEN, R?/AU
9 TSIEN, R?/IN
[illegible] TSIEN R? OR TSIEN, R?/AU,IN

fluorescent protein

[illegible] FLUORESCENT
[illegible] FLUORESCENCE
[illegible] FLUORESCENT
[illegible] FLUORESCENCE
[illegible] FLUORESCENT
[illegible] FLUORESCENCE
[illegible] FLUORESCENT
(PROTEIN OR PROTEINS)
L18 4046 FLUORESCENT PROTEIN
FLUORESCENT (W) PROTEIN

L19 ANSWER 3 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Recent advances in technology for measuring and manipulating cell signals.

L19 ANSWER 4 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Genetically encoded indicators of signal transduction and protein interaction.

L19 ANSWER 5 OF 35 BIOSIS COPYRIGHT 2000 BIOSIN
TI ***fluorescent*** ***protein*** sensors for detection of analytes.

L19 ANSWER 6 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Tandem ***fluorescent*** ***protein*** constructs.

L19 ANSWER 7 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Ligand-dependent interactions of coactivators steroid receptor coactivator-1 and peroxisome proliferator-activated receptor binding protein with nuclear hormone receptors can be imaged in live cells and are required for transcription.

L19 ANSWER 8 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Mitochondria-induced changes in intracellular pH regulate apoptosis.

L19 ANSWER 9 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI A genetically encoded, fluorescent indicator for cyclic AMP in living cells.

L19 ANSWER 10 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI GFP-based optical recording from a C. elegans sensory neuron.

L19 ANSWER 11 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Circular permutation and receptor insertion within green ***fluorescent*** ***proteins*** .

L19 ANSWER 12 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Assays for protein kinases using ***fluorescent*** ***protein*** substrates.

L19 ANSWER 13 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Assays for protein kinases using fluorescent.

L19 ANSWER 14 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI New molecules to peek and poke at signal transduction.

L19 ANSWER 15 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Dynamic redistribution of calmodulin in HeLa cells during cell division as revealed by a GFP-calmodulin fusion protein technique.

L19 ANSWER 16 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI [illegible]

L19 ANSWER 17 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI [illegible] ratio imaging with [illegible].

L19 ANSWER 18 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Dynamic and quantitative [illegible] measurements using improved [illegible].

L19 ANSWER 19 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI [illegible]

L19 ANSWER [illegible] BIOSIS COPYRIGHT [illegible] BIOSIS
TI GFP-mutagenesis and applications

L19 ANSWER 24 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Crystal structure and photodynamic behavior of the blue emission variant Y66H Y145F of green ***fluorescent*** ***protein*** .

L19 ANSWER 25 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Ratiometric indicators for Ca-2+ based on green ***fluorescent*** ***proteins*** and calmodulin.

L19 ANSWER 26 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Fluorescence imaging of cAMP gradients and protein localizations in living cells.

L19 ANSWER 27 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI On/off blinking and switching behaviour of single molecules of green ***fluorescent*** ***protein*** .

L19 ANSWER 28 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Green ***fluorescent*** ***proteins*** : Structures, photophysical mechanisms, and designed environmental sensitivities.

L19 ANSWER 29 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Structural basis for dual excitation and photoisomerization of the Aequorea victoria green ***fluorescent*** ***protein*** .

L19 ANSWER 30 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Measurement and manipulation of cell signals with photons and designed molecules.

L19 ANSWER 31 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Crystal structure of the Aequorea victoria green ***fluorescent*** ***protein*** .

L19 ANSWER 32 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Double labelling of subcellular structures with organelle-targeted GFP mutants in vivo.

L19 ANSWER 33 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Engineering green ***fluorescent*** ***protein*** for improved brightness, longer wavelengths and fluorescence resonance energy transfer.

L19 ANSWER 34 OF 35 BIOSIS COPYRIGHT 2000 BIOSIS
TI Understanding, improving and using green ***fluorescent*** ***proteins*** .

L19 ANSWER [illegible] BIOSIS COPYRIGHT [illegible] BIOSIS
[illegible] ***fluorescent*** ***protein*** .

=> d kwic 1-35

L19 ANSWER 1 OF 35 BIOSIS COPYRIGHT [illegible] BIOSIS
AU ***Tsien, R. Y.*** ; Miyawaki, A. ; Ikura, M. ; Inouye, S. ; [illegible] ; [illegible] ; Ai[illegible], S. B.

SOURCE: European Journal of Neuroscience, [illegible], N.
Supplement 11, pp. 1, print.
Meeting Info.: Meeting of the Federation of European
[illegible]
ISSN: [illegible].
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L1 ANSWER [illegible] BIOSIS COPYRIGHT [illegible] BIOSIS
TI ***Fluorescent*** ***protein*** sensors for detection of analytes.
AU ***Tsien, Roger Y. (1)*** ; Miyawaki, Atsushi
AB [illegible] fluorescent indicators including a binding protein moiety, a signal
fluorescent ***protein*** moiety, and an adaptor
fluorescent ***protein*** moiety are described. The binding
protein moiety has an analyte-binding region which binds an analyte and
causes the indicator to. . .
IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques
IT Chemicals & Biochemicals
fluorescent ***protein***
IT Methods & Equipment
analyte detection: detection method; ***fluorescent***
protein sensor: equipment
ACCESSION NUMBER: 2000:283023 BIOSIS
DOCUMENT NUMBER: PREV200000288023
TITLE: ***Fluorescent*** ***protein*** sensors for
detection of analytes.
AUTHOR(S): ***Tsien, Roger Y. (1)*** ; Miyawaki, Atsushi
CORPORATE SOURCE: (1) San Diego, CA USA
ASSIGNEE: The Regents of the University of California
PATENT INFORMATION: US 5998204 December 07, 1999
SOURCE: Official Gazette of the United States Patent and Trademark
Office Patents, (Dec. 7, 1999) Vol. 1229, No. 1, pp. No
pagination. e-file..
ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English

=> file medline embase caplus

FILE 'MEDLINE' ENTERED AT 17:47:19 ON 31 OCT 2001

FILE 'EMBASE' ENTERED AT 17:47:19 ON 31 OCT 2001
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FILE 'CAPLUS' ENTERED AT 17:47:19 ON 31 OCT 2001
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```
     FILE 'HCAPLUS' ENTERED AT [illegible] ON 31 OCT [illegible]
L[illegible]          [illegible] L[illegible]
L[illegible]          4 L[illegible] L3
L11          104 L7(S)L3
[illegible]           [illegible] AN [illegible]
[illegible]           [illegible] FHIBRIDIZATION LIBRARY
[illegible]           [illegible] L[illegible] AN [illegible]
L13            0 TSIEN/AU
L14            1 TANDEM FLUORESCENT PROTEIN
L15          [illegible]4  TSIEN R? OR TSIEN, R[illegible] AU,IN
L16          4[illegible]0 FLUORESCENT PROTEIN
L17           [illegible]1 L[illegible] AND L[illegible]

     FILE 'MEDLINE, EMBASE, CAPLUS' ENTERED AT [illegible] ON 31 OCT 2000
L[illegible]          [illegible] L[illegible]

=> [illegible]s\12

L21          [illegible] L7(S) L2

=> dup rem L21

PROCESSING COMPLETED FOR L21
L22          162 DUP REM L21 (155 DUPLICATES REMOVED)

=> d kwic 1,50,100,150,162


L22  ANSWER 1 OF 162  CAPLUS  COPYRIGHT 2000 ACS
TI   Yeast   ***two***  -  ***hybrid***   method for screening for
     protein-kinase   ***modulators***   in higher eukaryotic cells
IT   Phosphoproteins
     RL: AFG (Analytical reagent use); BPR (Biological process); ANST
     (Analytical study); BIOL (Biological study); PROC (Process); USES (Uses)
        (I.kappa.B; yeast   ***two***  -  ***hybrid***   method for screening
        for protein-kinase   ***modulators***   in higher eukaryotic cells)
IT   Antibodies
     RL: AFG (Analytical reagent use); ANST (Analytical study); USES (Uses)
        (anti-phosphorylated substrate; yeast   ***two***  -  ***hybrid***
        method for screening for protein-kinase   ***modulators***   in higher
        eukaryotic cells)
IT   Molecular association
        (of kinase substrate and binding partner; yeast   ***two***  -
        ***hybrid***   method for screening for protein-kinase
        ***modulators***   in higher eukaryotic cells)
IT   Animal cell
        (yeast   ***two***  -  ***hybrid***   method for screening for
        protein-kinase   ***modulators***   in higher eukaryotic cells)
IT   [illegible]
        [illegible]; yeast   ***two***  -  ***hybrid***   [illegible]; yeast   ***two***  -
        ***hybrid***   [illegible]
        ***modulators***   [illegible]
IT   [illegible]
     RL: AFG [illegible]; BPR [illegible]; ANST
     [illegible]; BIOL [illegible]; PROC [illegible]; USES [illegible]
        [illegible]; yeast
        ***two***  -  ***hybrid***   [illegible]
        ***modulators***   [illegible]
IT   [illegible]
     RL: [illegible]
```

L22 ANSWER 161 OF 162 MEDLINE [illegible]

AB . . . that the bovine herpesvirus 4 (BHV4) BORFF2 gene encodes a [illegible] that inhibits Fas- and TNFR1-induced apoptosis and contains death [illegible] domains (DEDs). Using the yeast ***two*** - ***hybrid*** system, we found that the BHV4 BORFF2 protein interacts with the procaspase-8. Furthermore, we show that BHV4 BORFF2 is. . .

L22 ANSWER 16 OF 162 MEDLINE [illegible]

AB Using the yeast ***two*** ***hybrid*** system and overlay assays we identified a putative rho[illegible] ***effector*** , Citron, which interacts with the GTP-bound forms of the small rho[illegible] GTPases rho, rac, and cdc42, but not with rho[illegible]. Extensive homologies to known proteins. . . long coiled-coil domain region including a leucine zipper and the rho[illegible] binding site. We recently identified three others putative rho ***effectors*** characterized by a common rho binding motif. Citron does not share this motif and displays a distinctive protein organization, thus. . .

L22 ANSWER 162 OF 162 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.

AB ***Two*** ***hybrid*** species of hemoglobin M Iwate exist: .alpha.2(Mmet).beta.(met).beta.(deoxy) and .alpha.2(Mmet).beta.2(deoxy). These species differ in their ligand and ***effector*** binding properties. The .alpha.2(Mmet).beta.(met).beta.(deoxy) hybrid is characterized by a Bohr effect, while the Hill coefficient is n=1.00. The energy of. . .

=> d abs 1

L22 ANSWER 1 OF 162 CAPLUS COPYRIGHT 2000 ACS

AB The invention concerns a method for yeast screening of protein-kinase modulators specific for higher eukaryotic cells, including human cells, characterized in that it consists of: (a) expressing the substrate(s) of said protein-kinases and the interacting partner(s) specific for said protein-kinase substrate(s) in a double-hybrid system in Saccharomyces cerevisiae in a selective culture medium in the presence of potential inhibiting agents of phosphorylation-dependent interactions of said substrate(s) with their specific partners; (b) screening in said double-hybrid system for said protein-kinase inhibitors; and (c) detg. the specificity of the inhibitors obtained in step (b) by reaction with an antibody specific for the phosphorylated form of the substrates. Thus, the method was demonstrated using the interaction of I.kappa.B.alpha. (fused to the Gal4 transactivation domain) with human .beta.TrCP (fused to the LexA DNA-binding domain). An antibody specific for phosphorylated I.kappa.B.alpha. indicated that I.kappa.B.alpha. was phosphorylated in Saccharomyces cerevisiae, even though yeast contains no protein kinase [illegible] the human TrCP.

L22 ANSWER 1 OF 162 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 2000:411044 CAPLUS

DOCUMENT NUMBER: 133:73648

TITLE: Yeast ***two*** - ***hybrid*** method to identify [illegible] protein-protein ***interactions*** in higher eukaryotic cells

[illegible]

[illegible] AT [illegible] WO 1998-EP6 A [illegible]
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE
FR [illegible] A [illegible] FR 1996-15841 19961219
ISI ENTRY AVAIL. INFO.: FR 1996-15841 19961219
REFERENCE COUNT: 4
REFERENCE(S): (1) Dana-Farber Cancer Institute Inc Us; WO 95/[illegible] A 1995
(2) Icos Corporation Us; WO 9[illegible] A 1995
(3) Mayo Found For Med Educat & Res Us; WO 9[illegible] A 1997
(4) Univ California; WO 9[illegible] A 1995

=> file embase medline caplus biosis

COST IN U.S. DOLLARS SINCE FILE ENTRY TOTAL SESSION
FULL ESTIMATED COST 1[illegible].50 15[illegible].70

DISCOUNT AMOUNTS FOR QUALIFYING ACCOUNTS SINCE FILE ENTRY TOTAL SESSION
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FILE 'BIOSIS' ENTERED AT 17:53:19 ON 31 OCT 2000
COPYRIGHT (C) 2000 BIOSIS(R)

=> psychrophile?

123 [illegible] PSYCHROPHILE?

=> expression library

124 8938 EXPRESSION LIBRARY

[illegible]

[illegible]

[illegible]

[illegible] [illegible] LIBRARY

[illegible]

[illegible]

DOCUMENT TYPE: [illegible]
LANGUAGE: [illegible]
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A1	[illegible]	WO [illegible]	[illegible]
W: [illegible]				
RW: [illegible]				
AU [illegible]	A1	[illegible]	AU [illegible]	[illegible]
EP [illegible]	A1	[illegible]	EP [illegible]	[illegible]
R: [illegible]				

PRIORITY APPLN. INFO.: US 1997-820113 19970315
WO 1998-US21496 19981013

REFERENCE COUNT: 5
REFERENCE(S):
(1) Chaudhuri; FEBS Lett 1995, V357(2), P221 CAPLUS
(2) Chiu; Proc Natl Acad Sci USA 1994, V91(26), P12574 CAPLUS
(3) Erickson; US 5525490 A 1996
(4) Mendelsohn; Curr Opin Biotechnol 1994, V5, P482 CAPLUS
(5) Yang; J Biol Chem 1995, V270(25), P15187 CAPLUS

AB The invention provides a method for screening new bio-active mols. for the ability to affect the interactions of proteins or other mols., whereby the interactions of said proteins/mols. are detected in vivo or in vitro. The method of the invention begins with the construction of DNA libraries which represent the collective genomes of naturally occurring microorganisms archived in cloning vectors that can be propagated in suitable prokaryotic hosts. Such microorganisms are preferably extremophiles, such as hyperthermophiles, ***psychrophiles*** , psychrotrophs, halophiles, and acidophiles. The method further involves contacting a bio-active compd. isolated from said library with a test protein linked to a DNA binding moiety or a second test protein linked to a transcriptional activation moiety and detg. the ability of said compd. to regulate the interaction of the first protein with the second, wherein said regulation enhances or inhibits the expression of a detectable protein. The invention offers the ability to screen for many types of bio-active compds., particularly those which are enhancers and inhibitors of protein-protein or other interactions, such as those between transcription factors and their activators or receptors and their cognate targets. In one embodiment, the methods are directed toward the discovery of possible antibiotics, anti-virals, anti-tumor agents, and regulatory proteins.

IT ***[illegible]*** ***library***
[illegible]

L [illegible] ***genomic*** ***libraries*** . Identification and
sequencing of the trpEG (D) operon.
AB **Random sequencing of cDNA and ***genomic*** ***libraries*** has**
been used to study the genome of the hyperthermophile Thermotoga maritima.
To date, [illegible] unique clones have been analyzed. . . . 18 trpG and 14 trpD
genes from other prokaryotes suggest that the Thermotoga trp genes resemble
corresponding genes from other ***thermophiles*** more closely than
expected.

L 11 ANSWER 3 OF 11 EMBASE COPYRIGHT (C) ELSEVIER SCI. B.V.
AB . . . with DNA fragments from four cyanobacterial species. We have
cloned the genes coding for subunits I and II from the ***genomic***
library of the thermophilic cyanobacterium Synech[illegible] and
determined the nucleotide sequence of the subunit II gene. The deduced
protein sequence . . . subunit IIs. The C. merolae subunit II does not
contain the cytochrome c activity that is present in Rapidii and
thermophiles .

L 11 ANSWER 3 OF 11 MEDLINE
AB . . . Pyrodictium occultum and Desulfurococcus mobilis among the
sequences in the database, indicating that NCL1 belongs to a cluster of
extreme ***thermophiles*** (Crenarchaeota) in the archaeal domain.
However, since the highest identity score was only 41.2%, it is suggested
that NCL1 may. . .
CT Archaea: CL, classification
*Archaea: GE, genetics
Archaea: IP, isolation & purification
Base Sequence
Cloning, Molecular
DNA, Bacterial
Genome, Bacterial
*** Genomic Library***
Molecular Sequence Data
Phylogeny
Polymerase Chain Reaction
Restriction Mapping
*RNA, Bacterial: GE, genetics
*RNA, Ribosomal, 16S: GE, genetics
. . .

L 11 ANSWER 4 OF 11 MEDLINE
TI Studies of the hyperthermophile Thermotoga maritima by random sequencing
of cDNA and ***genomic*** ***libraries*** . Identification and
sequencing of the trpEG (D) operon.
AB Random sequencing of cDNA and ***genomic*** ***libraries*** has
been used to study the genome of the hyperthermophile Thermotoga maritima.
To date, 175 unique clones have been analyzed. . . . 18 trpG and 14 trpD
genes from other prokaryotes suggest that the Thermotoga trp genes resemble
corresponding genes from other ***thermophiles*** more closely than
expected.
. . . [illegible], N.L.-H.H.
Amino Acid Sequence
Anthranilate Synthase: GE, genetics
Anthranilate Synthase: GE, genetics
Base Sequence
Cells
*DNA, Bacterial: GE, chemistry
Genomic Library
*Gram-Negative Anaerobic Bacteria: GE, genetics

...terium the cytochrome c moiety that is present in bacilli and
...thermophiles*** .

L31 ANSWER 9 OF 10 MEDLINE COPYRIGHT 2000 ACS
AB . . . mismatch in a widely used bacterium-specific 16S rRNA PCR amplification primer site. TP , which has also been reported to be ***thermophiles*** and split genes.
TI ...hyperthermophile ***library***
Construction and characterization of a DNA library of marine environmental phage DNA fragments representative of the entire viral community: the first planktonic bacteriophage

L31 ANSWER 10 OF 10 MEDLINE COPYRIGHT 2000 ACS
TI Studies of the hyperthermophile Thermotoga maritima by random sequencing of cDNA and ***genomic*** ***libraries***. Identification and sequencing of the trpEG (D) operon.
AB Random sequencing of cDNA and ***genomic*** ***libraries*** has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 175 unique clones have been analyzed. . . 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expected.

L31 ANSWER 9 OF 10 BIOSIS COPYRIGHT 2000 BIOSIS
TI Studies of the hyperthermophile Thermotoga maritima by random sequencing of cDNA and ***genomic*** ***libraries*** : Identification and sequencing of the trpEG (D) operon.
AB Random sequencing of cDNA and ***genomic*** ***libraries*** has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 175 unique clones have been analyzed. . . 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga rp genes resembled corresponding genes from other ***thermophiles*** more closely than expected.

L31 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2000 BIOSIS
AB. . . with DNA fragments from four cyanobacterial species. We have cloned the genes coding for subunits I and II from the ***genomic***
library of the thermophilic cyanobacterium Synechococcus vulcanus
...
...thermophiles*** .

...two yeast and 131

...TH YEAST AND 131

...H.
...: ...Biology Institute, University ... California, Los Angeles, CA 90024, United States
...: Journal of Molecular Biology, (1993) 231/4 (960-981).
ISSN: ...-2836 CODEN: JMOBAK
...: United Kingdom
... TYPE: Journal; Article
... SEGMENT: 114 Microbiology
029 Clinical Biochemistry
...: English
...: English
AB Rapid sequencing of cDNA and ***genomic*** ***libraries*** has been used to study the genome of the hyperthermophilic bacterium Thermotoga maritima. To date, 1 ... unique clones have been analyzed by comparing short sequence tags with known proteins in the PIR and GenBank databases. More than a significant proportion of sequences can be matched to previously identified proteins from non-Thermotoga sources. A high match rate was obtained from an oligo(dT)-primed cDNA library, where one-third of all unique sequences analyzed (21/60) shared high amino acid sequence similarity with proteins in the PIR and GenBank databases. Also, approximately one-third of the unique sequences from a second cDNA library (28/84), constructed with random oligo primers, could be matched to sequences in PIR and GenBank. Identification of genes from the oligo(dT)-primed cDNA library indicates that some Thermotoga mRNAs are polyadenylated. Genes have also been identified from a 1 to 2 kb genomic DNA library. Here, (3/21) of genomic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operon organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino acid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expected.

L31 ANSWER 2 OF 10 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 92041955 EMBASE
DOCUMENT NUMBER: 1992041955
TITLE: The cytochrome C oxidase genes in blue-green algae and characteristics of the deduced protein sequence for subunit II of the thermophilic cyanobacterium Synechococcus vulcanus.
AUTHOR: ... H.; Ishizuka M.; Sone N.
... AFFILIATION: Department ... Applied Chemistry, Faculty ... Science and Engineering, ... University, Tokyo, Japan
...: Biochimica et Biophysica Acta, (1992) ...
ISSN: ...-2728 CODEN: BBBAA
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
... SEGMENT: 029 Clinical Biochemistry
...: English
...: English

L31 ANSWER 3 OF 10 MEDLINE
ACCESSION NUMBER: 97128825 MEDLINE
DOCUMENT NUMBER: 97128825
TITLE: Cloning and sequencing of a gene encoding 16S ribosomal RNA from a novel hyperthermophilic archaebacterium NC12.
AUTHOR: Koshima M; Nishiko Y; Hasegawa M; Yamanishi A; Oshima T
CORPORATE SOURCE: Department of Molecular Biology, Tokyo University of Pharmacy and Life Science, Japan.
SOURCE: [illegible]
PUB. COUNTRY: Netherlands
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-D85038
ENTRY MONTH: 199703
AB A hyperthermophile NC12 was newly isolated from Noboribetsu hot spring. To characterize this organism, a gene coding for 16S rRNA was cloned and sequenced. The 16S rRNA sequence from NC12 shows the highest similarity with those from Pyrodictium occultum and Desulfurococcus mobilis among the sequences in the database, indicating that NC12 belongs to a cluster of extreme ***thermophiles*** (Crenarchaeota) in the archaeal domain. However, since the highest identity score was only 91.2%, it is suggested that NC1[illegible] may constitute a new genus

L31 ANSWER 4 OF 10 MEDLINE
ACCESSION NUMBER: 93294870 MEDLINE
DOCUMENT NUMBER: 93294870
TITLE: Studies of the hyperthermophile Thermotoga maritima by random sequencing of cDNA and ***genomic*** ***libraries*** . Identification and sequencing of the trpEG (D) operon.
AUTHOR: Kim C W; Markiewicz P; Lee J J; Schierle C F; Miller J H
CORPORATE SOURCE: Department of Microbiology and Molecular Genetics University of California, Los Angeles 90024..
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (1993 Jun 20) 231 (4) 960-81. Journal code: J6V. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Cancer Journals; Priority Journals
OTHER SOURCE: GENBANK-A30904; GENBANK-J01511; GENBANK-M33814; GENBANK-M36636; GENBANK-M55911; GENBANK-M65060; GENBANK-M93388; GENBANK-S66[illegible]1; GENBANK-X14960; GENBANK-X17149; GENBANK-X57853; PIR-A22626; PIR-A35116; PIR-A35284; PIR-A38989; PIR-B2493; PIR-B32840; PIR-C35115; PIR-D35[illegible]; PIR-[illegible]; PIR-[illegible]; PIR-[illegible]; PIR-[illegible]; PIR-[illegible]; PIR-[illegible]
ENTRY MONTH: [illegible]
AB [illegible]

[illegible] similar to Bacteria, Mit and Archaea
[illegible], but rather the closest attitude to eukaryotic [illegible].
Amino acid sequence comparison with 19 trpE, 18 trpG and 14 trpD genes
from other organisms suggest that the Thermotoga trp genes resemble
corresponding genes from other ***thermophiles*** more closely than
expected.

L31 ANSWER 5 OF 10 MEDLINE
ACCESSION NUMBER: [illegible] MEDLINE
DOCUMENT NUMBER: [illegible]
TITLE: The cytochrome C oxidase genes in blue-green algae and
their relationship with sequences in the mitochondrial
II of the thermophilic cyanobacterium Cyanidium caldarium.
AUTHOR: Lang B; Ishizaka H; Sato N
CORPORATE SOURCE: Department of Applied Chemistry, Faculty of Science and
Engineering, Chuo University, Tokyo, Japan..
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, [illegible]
N.Y.) 181 (1) [illegible].
Journal code: 9V8. ISSN: 0006-291X.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
OTHER SOURCE: GENBANK-S67470; GENBANK-S67146; GENBANK-S74367;
GENBANK-S67100; GENBANK-M64055; GENBANK-M64056;
GENBANK-M64057; GENBANK-M64058; GENBANK-M64059;
GENBANK-M64060
ENTRY MONTH: 199203
AB Blue-green algae (cyanobacteria) contain both primitive photosynthetic and respiratory systems in their membranes. The controversial genes coding for an alpha alpha 3-type cytochrome oxidase in cyanobacteria were examined. The DNA probe coding for the most conserved part of subunit I hybridized with DNA fragments from four cyanobacterial species. We have cloned the genes coding for subunits I and II from the ***genomic*** ***library*** of the thermophilic cyanobacterium Synechococcus vulcanus and determined the nucleotide sequence of the subunit II gene. The deduced protein sequence (327 amino acid residues) indicates that there are two hydrophobic segments near the N-terminus and a hydrophilic intermembrane domain containing ligands for CuA (the ESR-active Copper) similar to other subunit IIs. The S. vulcanus subunit II does not contain the cytochrome c moiety that is present in bacilli and ***thermophiles*** .

L31 ANSWER 6 OF 10 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:547256 CAPLUS
DOCUMENT NUMBER: 129:326484
TITLE: Screening of a fosmid library of marine environmental
[illegible] DNA [illegible] four [illegible]
[illegible]
AUTHOR(S): [illegible], Kevin J.; [illegible], Jeffrey L.;
[illegible], Edward F.; [illegible], Brian J.; [illegible],
Stephen J.
CORPORATE SOURCE: Department of Microbiology, [illegible],
Corvallis, OR, 97331, USA
SOURCE: Appl. Environ. Microbiol. [illegible], [illegible], [illegible]
CODEN: AEMIDF; ISSN: [illegible]
PUBLISHER: American Society for Microbiology
[illegible]
LANGUAGE: English

[redacted]
[redacted]
the trpEG (D) operon

AUTHOR(S): Kim, Choll Wan; Markiewicz, Peter; Lee, Jean J.; Setterle, Clark F.; Miller, Jeffrey H.

CORPORATE SOURCE: Mol. Biol. Inst., Univ. Calif. Los Angeles, CA, [redacted], USA

SOURCE: J. Mol. Biol. 1993, [redacted], [redacted]
CODEN: JMOBAK; ISSN: [redacted]

DOCUMENT TYPE: Journal

LANGUAGE: English

AB [redacted] has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 175 unique clones have been analyzed by comparing short sequence tags with known proteins in the PIR and GenBank databases. The authors find that a significant proportion of sequences can be matched to previously identified proteins from non-Thermotoga sources. A high match rate was obtained from an oligo(dT)-primed cDNA library, where one-third of all unique sequences analyzed (21/65) shared high amino acid sequence similarity with proteins in the PIR and GenBank databases. Also, approx. one-third of the unique sequences from a second cDNA library (28/89), constructed with random oligo primers, could be matched to sequences in PIR and GenBank. Identification of genes from the oligo(dT)-primed cDNA library indicates that some Thermotoga mRNAs are polyadenylated. Genes have also been identified from a 1 to 2 kb genomic DNA library. Here, (3/21) of genomic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operon organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino acid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resemble corresponding genes from other ***thermophiles*** more closely than expected.

L31 ANSWER 8 OF 10 CAPLUS COPYRIGHT 2000 ACS

ACCESSION NUMBER: 1993:2868 CAPLUS

DOCUMENT NUMBER: 118:2868

TITLE: The cytochrome c oxidase genes in blue-green algae and characteristics of the deduced protein sequence for subunit II of the thermophilic cyanobacterium Synechococcus vulcanus

AUTHOR(S): Tano, Hiroyuki; Ishimika, Mitio; Sone, Nobuhito

CORPORATE SOURCE: Fac. Biol. Eng., Tokyo Inst. Technol., Tokyo, 112, Japan

SOURCE: [redacted]
CODEN: [redacted]

DOCUMENT TYPE: [redacted]

LANGUAGE: English

AB [redacted] respiratory systems in their membranes. The [redacted] for an aa3-type cytochrome oxidase in cyanobacteria were exam[redacted]. The DNA probe coding for the most conserved part of subunit I hybridized with DNA fragments from four cyanobacterial species. [redacted] from thermophilic cyanobacterium S. vulcanus, and the [redacted]

[illegible]

AUTHOR(S): Kim, [illegible]; Markiewicz, P.; Ingraham, J.L.; **Schroeder, Clark E.; Miller, Jeffrey H.**

CORPORATE AUTHOR: (1) Mol. Biol. Inst., Dep Microbiol., Univ. California, Los Angeles, CA 90024 USA

SOURCE: Journal of Molecular Biology, (1993) Vol. 231, No. 4, pp. 960-981.
ISSN: 0022-2836.

DOCUMENT TYPE: Article

LANGUAGE: English

AB Random sequencing of cDNA and ***genomic*** ***libraries*** has been used to study the genome of the hyperthermophile Thermotoga maritima. To date, 1176 unique clones have been analyzed by comparing short sequence tags with known proteins in the PIR and GenBank databases. We find that a significant proportion of sequences can be matched to previously identified proteins from non-Thermotoga sources. A high match rate was obtained from a [illegible]-primed cDNA library, where one-third of all unique sequences analyzed (21/67) shared high amino acid sequence similarity with proteins in the PIR and GenBank databases. Also, approximately one-third of the unique sequences from a second cDNA library (78/252), constructed with random oligo primers, could be matched to sequences in PIR and GenBank. Identification of genes from the oligo(dT)-primed cDNA library indicates that some Thermotoga mRNAs are polyadenylated. Genes have also been identified from a 1 to 2 kb genomic DNA library. Here, (3/21) of genomic sequences analyzed could be matched to proteins in PIR and GenBank. One of the genomic clones had high sequence similarity to the tryptophan synthesis gene anthranilate synthase component I (trpE). Using this sequence tag, the Thermotoga trp operon was isolated and sequenced. The Thermotoga maritima trp operon is arranged with trpE forming an overlapping transcript with a second protein consisting of a fusion of anthranilate synthase component II (trpG) and anthranilate phosphoribosyltransferase (trpD). With regard to the fusion, the operon organization is similar to Escherichia coli and Salmonella typhimurium, but lacks the classic attenuation system of enteric bacteria. Amino acid sequence comparisons with 19 trpE, 18 trpG and 14 trpD genes from other organisms suggest that the Thermotoga trp genes resembled corresponding genes from other ***thermophiles*** more closely than expected.

L31 ANSWER 10 OF 10 BIOSIS COPYRIGHT 2000 BIOSIS
ACCESSION NUMBER: 1991:76632 BIOSIS
DOCUMENT NUMBER: BA91:45087
TITLE: THE CYTOCHROME C OXIDASE GENES IN BLUE-GREEN ALGAE AND CHARACTERISTICS OF THE DEDUCED PROTEIN SEQUENCE FOR SUBUNIT II OF THE THERMOPHILIC CYANOBACTERIUM SYNECHOCOCCUS-VULCANUS.
AUTHOR(S): TANO H; ISHIZUKA M; SONE N
CORPORATE AUTHOR: DEPT. APPLIED CHEMISTRY, FACULTY SCIENCE ENGINEERING, CHUO UNIVERSITY, BUNKYO-KU, TOKYO-TO, 112 JPN, JAPAN.
SOURCE: BIOCHEM BIOPHYS RES COMMUN, (1991) 174 (1), 44-49.
ISSN: 0006-291X. [illegible]
DOCUMENT TYPE: BA; FA
LANGUAGE: English
AB Blue-green algae (cyanobacteria) contain both primitive photosynthetic and respiratory systems in their membranes. The [illegible] gene coding for an aa3-type cytochrome oxidase in cyanobacteria were examined. The DNA probe [illegible] for the most conserved part of subunit I hybridized with DNA [illegible] in cyanobacterial genomes. By [illegible] of the gene [illegible] subunit I and II in the ***genomic*** ***library***

[illegible] syntax is:
N XX ---- [illegible] the number of postings.
DISPLAY Display statistics of the search
ENTER SEARCH STATUS PYTION (NONE), STATUS, OR HISTORY

[illegible] CA1 DNA LIGASE/PHILI
[illegible] +PF+ DNA EXPRESSION LIBRARY
[illegible] DNA L4 AND L1

[illegible]

L23 ANSWER 1 OF 665 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI A DNA ligase from the ***psychrophile*** Pseudoalteromonas haloplanktis gives insights into the adaptation of proteins to low temperatures.

L23 ANSWER 200 OF 665 CAPLUS COPYRIGHT 2000 ACS
TI Effect of low temperature on microbial growth: lowered affinity for substrates limits growth at low temperature

L23 ANSWER 400 OF 665 BIOSIS COPYRIGHT 2000 BIOSIS
TI Cloning of phosphatase I gene from a ***psychrophile*** , Shewanella sp., and some properties of the recombinant enzyme.

L23 ANSWER 600 OF 665 BIOSIS COPYRIGHT 2000 BIOSIS
TI THE MICROBIOLOGY OF POLONY.

=> genomic library and l23

L34 1 GENOMIC LIBRARY AND L23

=> screening and l23

L35 2 SCREENING AND L23

=> d kwic

L35 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2000 ACS
TI ***Screening*** extremophiles for novel compounds which regulate biological interactions
AB The invention provides a method for ***screening*** new bio-active mols. for the ability to affect the interactions of proteins or other mols., whereby the interactions of said. . . . arrived in cloning [illegible] ***psychrophile*** , psychrotrophic, mesophilic, and extremophilic. In [illegible]
[illegible]
TI [illegible] ***screening*** DNA library [illegible]
IT Transcription factors
RL: [illegible]
DNA library from; ***screening*** extremophiles for novel compds. which regulate biol. interactions)
IT Transcription factors
RL: [illegible]

(from Streptomyces rimosus; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Microorganism
(psychrophilic; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Green fluorescent protein
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(reporter; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Archaebacteria (Archaea)
(halo ***screening***
(thio
(ultr
Marine microorganism
(***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Luciferases
RL: ANT (Analyte); ANST (Analytical study)
(***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Microorganism
(thermophilic; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT Microorganism
(uncultivated; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

IT 9001-78-9, Alkaline phosphatase 9014-00-0, Luciferase 9031-11-2, .beta.-Galactosidase 9040-07-7, Chloramphenicol acetyl transferase
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(reporter; ***screening*** extremophiles for novel compds. which regulate biol. interactions)

=> d kwic ibib 2

L35 ANSWER 2 OF 2 BIOSIS COPYRIGHT 2000 BIOSIS
IT Industry
chemical industry
IT Miscellaneous Descriptors
BIOCHEMICAL ENGINEERING; BIOTECHNOLOGY; ENVIRONMENT; ENZYMES; EXTREME CONDITIONS; FERMENTATION; MEDIA; ***PSYCHROPHILES*** ; SCALE-UP; ***SCREENING*** ; THERMOPHILES
ACCESSION NUMBER: 1995:323814 BIOSIS
DOCUMENT NUMBER: PREV199598338114
TITLE: Bioscreening novel bacteria, with an eye to biotechnological applications.
AUTHOR(S): Horikoshi, Koki
CORPORATE SOURCE: Japan Marine Sci. & Tech. Ctr., Yokosuka, Japan
SOURCE: Bioscience, Biotechnology, and Biochemistry, (1995) Vol. 59, No. 5, pp. 727-735.
ISSN: 0916-8451.
DOCUMENT TYPE: General Review
LANGUAGE: English

ENTER L# LIST OR END:L37

L# DISPLAY 4 MEDLINE FOR L37
L## 4 L37 REM L## , DUPLICATES REMOVED

? s awl ? tf

L## ANSWER 1 OF 4 MEDLINE
AB . . . positive selection for mutants of the human histone
hairpin-binding protein (HBP) capable of interacting with non-canonical
hairpins and in a ***negative*** ***selection*** for
loss-of-binding mutants. Interestingly, all mutations from the positive
selection are located in the N- and C-terminal regions flanking a. . .
. . .
ME, metabolism
RNA-Binding Proteins: CH, chemistry
*RNA-Binding Proteins: GE, genetics
*RNA-Binding Proteins: ME, metabolism
Saccharomyces cerevisiae: GE, genetics
Selection (Genetics)
*** Two Hybrid System Techniques***

L38 ANSWER 2 OF 4 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.DUPLICATE 1
TI New tools for protein linkage mapping and general ***two*** -
hybrid screening.
AB The ***two*** - ***hybrid*** system has proved to be a facile method
for detecting and analyzing protein-protein interactions. An expanded
application of this system,. . . new strains and vectors that will
allow for more efficient screening. The strains contain a GAL1-URA3
reporter for positive and ***negative*** ***selection*** , as well
as a UAS(G)-lacZ reporter. The strains are of opposite mating types,
permitting libraries present in one strain to. . . plasmids, despite
significantly lower protein levels. In addition to protein linkage
mapping, these reagents should be generally useful in standard ***two***
- ***hybrid*** applications.

L38 ANSWER 3 OF 4 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.DUPLICATE 2
TI Genetic characterization of a mammalian protein-protein interaction domain
ry using a yeast reverse ***two*** - ***hybrid*** system.
AB . . . protein-protein interactions to be selected from large libraries
of randomly generated mutant alleles. The strategy, based on a yeast
reverse ***two*** - ***hyorid*** system, involves a first-step
negative ***selection*** for mutations that affect

L## ANSWER 4 OF 4 [illegible]
TI A new version of the ***two*** - ***hybrid*** assay for detection
protein-protein interactions
AB The yeast ***two*** - ***hybrid*** system originally developed by
Fields and Song is a powerful in vivo assay to detect protein-protein

(Uses)
[illegible] response element; new version of the ***two*** -
hybrid assay for detection of protein-protein interactions)

IT Genetic methods
(new version of the ***two*** - ***hybrid*** assay for detection of protein-protein interactions)

IT Proteins, biological studies
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(new version of the ***two*** - ***hybrid*** assay for detection of protein-protein interactions)

IT Receptors
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(estrogen, DNA-binding domain; new version of the ***two*** - ***hybrid*** assay for detection of protein-protein interactions)

=> d ibib 1,4

L38 ANSWER 1 OF 4 MEDLINE
ACCESSION NUMBER: 2000175724 MEDLINE
DOCUMENT NUMBER: 20175724
TITLE: Positive and negative mutant selection in the human histone hairpin-binding protein using the yeast three-hybrid system.
AUTHOR: Martin F; Michel F; Zenklusen D; Muller B; Schumperli D
CORPORATE SOURCE: Abteilung fur Entwicklungsbiologie, Zoologisches Institut der Universitat Bern, Baltzerstrasse 4, 3012 Bern, Switzerland.
SOURCE: NUCLEIC ACIDS RESEARCH, (2000 Apr 1) 28 (7) 1594-603.
Journal code: O8L. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Cancer Journals
ENTRY MONTH: 200007
ENTRY WEEK: 20000701

L38 ANSWER 4 OF 4 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 1995:487672 CAPLUS
DOCUMENT NUMBER: 123:75824
TITLE: A new version of the ***two*** - ***hybrid*** assay for detection of protein-protein interactions
AUTHOR(S): Le Douarin, Bertrand; Pierrat, Benoit; vom Baur, Elmar; Chambon, Pierre; Losson, Regine
CORPORATE SOURCE: Inst. Genetique et de Biol. Mol. Cell., Coll. de France, Strasbourg, Fr.
SOURCE: Nucleic Acids Res. [illegible]
CODEN: NARHAD; ISSN: [illegible]
DOCUMENT TYPE: Journal
LANGUAGE: English

=> d ibib [illegible]

[illegible]

LANGUAGE: English
SUMMARY LANGUAGE: English

L40 ANSWER 1 OF 1 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.DUPLICATE 1
ACCESSION NUMBER: 96179005 EMBASE
DOCUMENT NUMBER: 1996179005
TITLE: Genetic characterization of a mammalian protein-protein interaction domain by using a yeast reverse ***two*** - ***hybrid*** system.
AUTHOR: Vidal M.; Braun P.; Chen E.; Boeke J.D.; Harlow E.
CORPORATE SOURCE: Building 149, Massachusetts Gen. Hosp. Cancer Ctr., 13th Street,Charlestown, MA 02129, United States
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1996) 93/19 (10321-10326). ISSN: 0027-8424 CODEN: PNASA6
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 003 Human Genetics
029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

=> (short j? or short, j?)/au,in

'IN' IS NOT A VALID FIELD CODE
'IN' IS NOT A VALID FIELD CODE
L39 1066 (SHORT J? OR SHORT, J?)/AU,IN

=> l39 and two hybrid

L40 1 L39 AND TWO HYBRID

=> d kwic

L40 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2000 ACS
IN ***Short, Jay M.***
AB . . . single-chain antibodies. Shuffling can also be used to recombinatorially diversify a pool of selected library members obtained by screening a ***two*** - ***hybrid*** screening system to identify library members which bind a predetd. polypeptide sequence.

structure analysis
amino terminal sequence
animal cell
article
carboxy terminal sequence
chicken
crystal structure
hydrophobicity
molecular recognition
nonhuman
nuclear magnetic resonance
peptide synthesis
priority journal
protein domain
protein secondary structure
signal transduction
vertebrate
vertebrate

L43 ANSWER 2 OF 2 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
AU Ward A.J.; ***Short J.H.***
DT Medical Descriptors:
****protein protein interaction***
article
complex formation
molecular dynamics
nuclear magnetic resonance
priority journal
protein binding

> d abs tot

L43 ANSWER 1 OF 2 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
AB The interaction of apocalmodulin (apoCaM) with a peptide (Neuro(p)) based on the primary sequence of the calmodulin-binding domain of neuromodulin has been studied by nuclear magnetic resonance (NMR) methods. The NMR spectra of both apocalmodulin and its 1:1 complex with the Neuro(p) peptide have been assigned by triple resonance and nuclear Overhauser effect- (NOE-) based strategies. ApoCaM displays many of the same basic structural features as calcium-saturated calmodulin. Analysis of observed chemical shifts and patterns of NOEs on the main chain indicates extensive and regular secondary structure throughout the N-terminal domain. In contrast, the helices of the C-terminal domain are somewhat irregular and are dynamically averaged. The EF-hands are intact in the N-terminal domain with the loops forming a short antiparallel .beta. sheet. Under low-salt [illegible] helix-loop-helix EF-hand motifs are present in the C-terminal domain [illegible] NOEs. The apoCaM-Neuro(p) complex [illegible] with the Neuro(p) peptide [illegible] with the apoCaM N-terminal domain. The peptide secondary structure and tertiary orientation appears to be [illegible] in the complex. Stoichiometric titration of the apoCaM.cntdot.Neuro(p) complex with calcium indicates that the C-terminal domain EF-hands have a higher affinity for calcium than N-terminal domain EF-hands. Thus, this complex [illegible] unique opportunity to examine the [illegible] and thermodynamic properties of calcium-binding and calcium-independent [illegible] within the same [illegible].

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     FILE 'BIOSIS' ENTERED AT [illegible]
L9              0 L7(W)L3
L10             4 L7 (5W) L3
L11           [illegible]
L12             [illegible]
L13           [illegible]
L14           [illegible]
L15           [illegible]
L16             [illegible]
L17           [illegible]
L18           [illegible]
L19           [illegible]

     FILE 'MEDLINE, EMBASE, CAPLUS' ENTERED AT [illegible]
L20         [illegible]
L21           [illegible]
L22           162 DUP REM L21 (155 DUPLICATES REMOVED)

     FILE 'EMBASE, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 17:58:19 ON 31 OCT 2000
L23           665 PSYCHROPHILE?
L24          [illegible] EXPRESSION LIBRARY
L25             [illegible] L24 AND L23
L26         21198 GENOMIC LIBRARY
L27             [illegible] L25 AND L26
L28           218 EXTREMOPHILE?
L29             [illegible] L26 AND L28
L30          1268 THERMOPHILES
L31            10 L30 AND L26
L32             0 TWO YEAST AND L31
L33             0 TWO HYBRID AND L31
L34             1 GENOMIC LIBRARY AND L23
L35             2 SCREENING AND L23
L36          5627 NEGATIVE SELECTION
L37            12 L36 AND TWO HYBRID
L38             4 DUP REM L37 (6 DUPLICATES REMOVED)
L39          1066 (SHORT J? OR SHORT, J?)/AU,IN
L40             1 L39 AND TWO HYBRID
L41         37393 PROTEIN PROTEIN INTERACTION?
L42             2 L41 AND L39
L43             2 DUP REM L42 (0 DUPLICATES REMOVED)

[illegible]

  3 FILES SEARCHED...
L44          2865 L6

[illegible]

     FILE 'CAPLUS'...
[illegible]

[illegible]

PROTEIN 1 IS APPROXIMATELY [illegible] COMPLETE FOR L45
PROCESSING COMPLETED FOR L45
[illegible] DUP REM L45 [illegible] DUPLICATES REMOVED)

[illegible]
```

. . . and carrying one type each of the fusion proteins are mated together. Productive interactions between the two halves of the ***protein*** - ***protein*** ***interactions*** lead to the reconstitution of the transcriptional activator, which in turn leads to the activation of a reporter gene contg.. . . carried out for two or more populations of proteins. The differences in the genes encoding the proteins involved in the ***protein*** - ***protein*** ***interactions*** are characterized, thus identifying the identities of specific ***protein*** - ***protein*** ***interactions*** , and the genes encoding the interacting proteins, relevant to a particular tissue, stage or disease. Furthermore, inhibitors that interfere with these ***protein*** - ***protein*** ***interactions*** are identified by their ability to inactivate a reporter gene. The screening for such inhibitors can be in a multiplexed. . . methods and systems provide for identification of the genes coding for detected interacting proteins, for assembling a unified database of ***protein*** - ***protein*** ***interaction*** data, and for processing this unified database to obtain protein interaction domain and protein pathway information. The method was used. . .

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(ADE2, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(CAN1; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(CUP1, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(CYH2; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Protein motifs
(DNA binding domain, fusion proteins contg.; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Proteins, specific or class
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(fusion proteins, DNA-binding; assay of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(BIS3, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(LEU2, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(LYS2, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Proteins, specific or class
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(R4; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Genetic methods
(SEQ-QEA; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(TRP1, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(VP16, of herpes simplex virus; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors)

inhibitors)
IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(gene AseN; identification and comparison of ***protein*** -
protein ***interactions*** and identification of
inhibitors)
IT Eukaryotic ribosomal proteins
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(gene RAB, interaction with YPR1; identification and comparison of
protein - ***protein*** ***interactions*** and
identification of inhibitors)
IT Phosphoproteins
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(gene -rat, interaction with Ras of; identification and comparison of
protein - ***protein*** ***interactions*** and
identification of inhibitors)
IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(gene lexA, DNA binding domain of; identification and comparison of
protein - ***protein*** ***interactions*** and
identification of inhibitors)
IT Animal tissue
Disease, animal
Transcriptional regulation
(identification and comparison of ***protein*** - ***protein***
interactions and identification of inhibitors)
IT Fusion proteins (chimeric proteins)
Promoter (genetic element)
Proteins, general, biological studies
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(identification and comparison of ***protein*** - ***protein***
interactions and identification of inhibitors)
IT Ras proteins
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(interaction with Raf of; identification and comparison of
protein - ***protein*** ***interactions*** and
identification of inhibitors)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use,
unclassified); BIOL (Biological study); USES (Uses)
(lacZ, reporter gene; identification and comparison of ***protein***
- ***protein*** ***interactions*** and identification of
inhibitors)
IT Rabbit
(gene Rab; identification and comparison of ***protein*** -
protein ***interactions*** and identification of
inhibitors)
IT Protein Phosphatase
Saccharomyces cerevisiae
Yeast
(gene ***protein*** - ***protein*** ***interactions*** assay
carbon-14 in; identification and comparison of ***protein*** -
protein ***interactions*** and identification of
inhibitors)
(gene ; identification and comparison of ***protein*** -
protein ***interactions*** and identification of
inhibitors)

IT Assay methods
[illegible] system; identification [illegible]
of ***protein*** - ***protein*** ***interactions*** and
identification of inhibitors
IT [illegible]
RL: BSU (Biological study, unclassified); BIOL (Biological study); USES
(Uses)
interaction with KDK of; identification and comparison of
protein - ***protein*** ***interactions*** and
identification of inhibitors
IT [illegible], L-Leucine, biological studies [illegible], L-Histidine,
biological studies [illegible], L-Tryptophan, biological studies
[illegible]
RL: BSU (Biological use, unclassified); BIOL (Biological study); USES
(Uses)
selecting agent; identification and comparison of ***protein*** -
protein ***interactions*** and identification of
inhibitors
IT [illegible] unclaimed DNA [illegible] unclaimed DNA
225626-81-3 239240-98-6 243927-87-9, PN: US5972693 SEQID: 1 unclaimed
DNA 243928-13-4, PN: US5972693 SEQID: 2 unclaimed DNA [illegible],
PN: US5972693 SEQID: 42 unclaimed DNA 249261-61-8, PN: US5972693 SEQID:
61 unclaimed DNA 249261-62-9, PN: US5972693 SEQID: 62 unclaimed DNA
249261-63-0, PN: US5972693 SEQID: 63 unclaimed DNA 249261-64-1, PN:
US5972693 SEQID: 64 unclaimed DNA 249261-65-2, PN: US5972693 SEQID: 65
unclaimed DNA 249261-66-3, PN: US5972693 SEQID: 66 unclaimed DNA
249261-67-4, PN: US5972693 SEQID: 67 unclaimed DNA 249261-70-9, PN:
US5972693 SEQID: 69 unclaimed DNA 249261-71-0, PN: US5972693 SEQID: 70
unclaimed DNA 249301-68-6, PN: US5972693 SEQID: 59 unclaimed DNA
266333-78-1, 1: PN: US6057101 SEQID: 8 unclaimed DNA 266333-79-2, 2: PN:
US6057101 SEQID: 9 unclaimed DNA 266333-79-2, 3: PN: US6057101 SEQID: 10
unclaimed DNA 266333-79-3, 4: PN: US6057101 SEQID: 11 unclaimed DNA
266333-80-6, 5: PN: US6057101 SEQID: 12 unclaimed DNA 266333-81-7, 6:
PN: US6057101 SEQID: 13 unclaimed DNA 266333-82-8, 7: PN: US6057101
SEQID: 14 unclaimed DNA 266333-83-9, 8: PN: US6057101 SEQID: 15
unclaimed DNA 266333-84-0, 9: PN: US6057101 SEQID: 16 unclaimed DNA
266333-85-1 266333-86-2 266333-87-3 266333-88-4 266333-89-5
266333-90-8 266333-91-9 266333-92-0 266333-93-1 266333-94-2
266333-95-3 266333-96-4 266333-97-5 266333-98-6 266333-99-7
266334-01-3 266334-02-4 266334-03-5 266334-04-6 266334-05-7
266334-06-8 266334-07-9 266334-08-0 266334-09-1 266334-10-4
266334-11-5 266334-12-6 266334-13-7 266334-14-8 266334-15-9
266334-16-0 266334-17-1 266334-18-2 266334-19-3 266334-20-6
266334-21-7 266334-22-8 266334-23-9 266334-24-0 266334-25-1
266334-26-2 266334-27-3 266334-28-4 266334-29-5 266334-30-9
266334-31-0 266334-32-1 266334-33-2 266334-34-3
[illegible]
266334-65-3 266334-66-4 266334-67-5 266334-68-6 266334-69-7
266334-70-0
RL: PRP (Properties)
[illegible]
protein - ***protein*** ***interactions*** and
identification of inhibitors

mammalian ***two*** - ***hybrid*** assays. Direct physical interactions of CBP/p300 with p60 were demonstrated by glutathione S-transferase fusion protein binding and coimmunoprecipitation/Western blot studies. . .
CT Medical Descriptors:
*transcription regulation
animal cell
article
cell line
controlled study
drosophila
endothelium cell
gene activation
gene overexpression
human
human cell
immune response
inflammation: EC, etiology
nonhuman
priority journal
protein protein interaction
reporter gene
*cyclic amp responsive element binding protein: EC, endogenous compound
*endothelial leukocyte adhesion molecule 1
*immunoglobulin enhancer binding protein: EC,. . .

L46 ANSWER 200 OF 681 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.DUPLICATE 60
SO Journal of Neuroscience Research, (1997) 48/5 (407-424).
Refs: 37
ISSN: 0360-4012 CODEN: JNREDK
AB . . . is involved in the CNS, we screened molecules that directly associate with Fyn in neonatal mouse brain by using a ***two*** - ***hybrid*** yeast system. We isolated five cDNA clones with strong and reproducible Fyn-binding activity. Sequence analyses revealed that three of them. . .
CT Medical Descriptors:
*brain
*signal transduction
animal tissue
article
dna library
enzyme binding
molecular cloning
mouse
newborn
nonhuman
priority journal
protein protein interaction
yeast
*cyclic amp responsive element binding protein
*tyrosine kinase

L47 ANSWER [illegible] EMBASE COPYRIGHT [illegible] ELSEVIER SCI. B.V.DUPLICATE [illegible]
SO [illegible] Journal of Biological Chemistry, [illegible]
ISSN: 0021-9258 CODEN: JBCHA3
AB LIM domains, Cys-rich motifs containing approximately 50 amino acids found in a variety of proteins, are proposed to direct ***protein*** - ***protein*** ***interaction***. To identify structural [illegible]

priority journal
protein structure
sequence analysis
*protein tyrosine kinase

L46 ANSWER [illegible] OF 681 EMBASE COPYRIGHT [illegible] ELSEVIER SCI. B.V.
SO Journal of Biological Chemistry, [illegible].
ISSN: [illegible] CODEN: [illegible]
AB . . . protein adenomatous polyposis coli. Abl, which appears to have a
role in neuronal cell proliferation. We have used the yeast ***two***
- ***hybrid*** method to show that Dab1, a mammalian
[illegible]'s neuronal adaptor protein Disabled
Western blotting of. . .
CT Medical Descriptors:
****protein protein interaction***
animal tissue
article
brain tissue
cell interaction
controlled study
endothelium cell
epithelium cell
immunoblotting
immunofluorescence microscopy
mouse
nonhuman
priority journal
rat
yeast
*actin binding protein: EC, endogenous compound
*beta catenin: EC, endogenous compound
*fascin:. . .

L46 ANSWER 500 OF 681 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Journal of Biological Chemistry, (1995) 270/37 (21461-21463).
ISSN: [illegible] CODEN: JBCHA3
AB . . . H., and Paolo DiFiore, P. (1995) Science 267, 381-383). Using the
cytoplasmic domain of Ret as bait in a yeast ***two*** - ***hybrid***
screen of a mouse embryonic library, it was discovered that the src
homology 2 (SH2) domain containing protein Grb10 bound. . .
CT Medical Descriptors:
****protein protein interaction***
article
nonhuman
priority journal
protein analysis
protein binding
[illegible]

L47 ANSWER [illegible]
SO ***[illegible]*** - ***protein*** ***[illegible]*** : Methods in
Molecular Biology.
CT Molecular Medicine Reviews, [illegible].
ISSN: [illegible] CODEN: MMREV3
AB . . . by the yeast two-hybrid system. This system is
[illegible] ***[illegible]*** -

[illegible]
[illegible]
gel filtration
[illegible]
[illegible]
[illegible]
histology
radioligand
binding affinity
[illegible]
[illegible]
human
hybrid
[illegible]
[illegible]
[illegible]
nonhuman
phenotype
plasma
polyacrylamide gel electrophoresis
review
sedimentation rate
*adenosine triphosphatase: EC, endogenous compound
*cyclic amp dependent protein kinase: EC, endogenous compound
*glutathione. . .

=> d ibib 1

146 ANSWER 1 OF 681 CAPLUS COPYRIGHT 2000 ACS
ACCESSION NUMBER: 2000:283960 CAPLUS
DOCUMENT NUMBER: 132:315571
TITLE: Identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of inhibitors
INVENTOR(S): Nandabalan, Krishnan; Rothberg, Jonathan Mark; Yang, Meijia; Knight, James Robert; Kalbfleisch, Theodore Samuel
PATENT ASSIGNEE(S): Curagen Corporation, USA
SOURCE: U.S., 161 pp., Cont.-in-part of U.S. Ser. No. 663,824.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
[illegible]	A	[illegible]	[illegible]	[illegible]
[illegible]	A	[illegible]	[illegible]	[illegible]
[illegible]	A2	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]

PRIORITY APPLN. INFO.:
REFERENCE COUNT: 14
REFERENCE(S):
(1) Brent; US [illegible] CAPLUS
(2) Fields; US [illegible] CAPLUS
(3) Lehner; US [illegible] CAPLUS
(4) [illegible]; US [illegible] CAPLUS
(5) Vojtek et al.; [illegible], [illegible]

[illegible] - 'AN' [illegible] 'LIA' [illegible] INHIBITOR'
[illegible] INHIBIT[illegible]

[illegible]

L47 ANSWER 1 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
[illegible] of the National Academy of Sciences of the United States of America, [illegible]
Refs: 49
[illegible] CODEN: PNASA6
AB . . . from the dorsal-ventral axis in the Drosophila embryo. Upon activation of the transmembrane receptor Toll, a total loss-of-function mutation in the intracellular protein Tube or the serine/threonine kinase Pelle are required to relay the signal from Toll to the Dorsal-Cactus complex. In a yeast ***two*** - ***hybrid*** assay, we found that both Tube and Pelle interact with Dorsal. We confirmed these interactions in an in vitro binding. . .
CT Medical Descriptors:
*embryo development
signal transduction
protein targeting
cell nucleus
protein protein interaction
drosophila
nonhuman
embryo
article
priority journal
*protein
*polymer
membrane receptor

L47 ANSWER 2 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI A yeast genetic system for selecting small molecule ***inhibitors*** of ***protein*** - ***protein*** ***interactions*** in nanodroplets.
SO Proceedings of the National Academy of Sciences of the United States of America, (1997) 94/25 (13396-13401).
Refs: 49
ISSN: 0027-8424 CODEN: PNASA6
AB . . . networks of molecular interactions. Dissection of their role most commonly is achieved by using genetic mutations that alter, for example, ***protein*** - ***protein*** ***interactions*** . Small molecules that accomplish the same result would provide a powerful complement to the genetic approach, but it generally is. . . polymer beads. Here, we describe a genetic system compatible with split-pool synthesis that allows [illegible] ***inhibitors*** [illegible] ***protein*** - ***protein*** ***interactions*** [illegible] nanodroplets, prepared by a [illegible] ***two*** - ***hybrid*** assay. Disruption of the interaction by a small molecule [illegible] This system enables a general method for selecting cell-permeable [illegible] ***protein*** - ***protein*** ***interactions*** in intact cells.
CT Medical Descriptors:

[illegible]
[illegible]
[illegible]
[illegible]
[illegible]
[illegible]

L47 ANSWER 3 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
JO Molecular Endocrinology, [1994] 1141- (1411-1421).
Refs: 44
ISSN: [illegible] CODEN: MOENEN
AB In a first series of experiments done in the yeast ***two*** - ***hybrid*** system, we investigated the nature of ***protein*** - ***protein*** interactions between the regulatory subunit of phosphatidylinositol 3-kinase (PI 3-kinase), p85 (PIK), and several of its potential signaling partners. The [illegible] between . . . tyrosine kinase and involved both p85(PIK) SH2 domains. Interaction between p85(PIK) and IGF-1R was seen not only in the yeast ***two*** - ***hybrid*** system, but also using in vitro binding and coimmunoprecipitation of lysates from IGF-1 stimulated 293 cells overexpressing p85(PIK). Further, IGF-1. . . p85(PIK) with insulin receptor substrate-1 and with IGF-1R was dependent on PI 3-kinase, since it was increased by wortmannin, an ***inhibitor*** of PI 3-kinase. Further, by deleting amino acids [illegible] of p85(PIK) inter-SH2 domain, we engineered a p85(PIK) mutant unable to. . .
CT Medical Descriptors:
*signal transduction
animal cell
article
enzyme subunit
feedback system
glucose transport
hormone receptor interaction
male
nonhuman
priority journal
protein binding
protein protein interaction
rat
*phosphatidylinositol 3 kinase
*somatomedin c
protein subunit
wortmannin

L47 ANSWER 4 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
JO Journal of Biological Chemistry, [1997] 272(45) [28433-28414].
Refs: 68
ISSN: [illegible] CODEN: JBCHA3
AB . . . [illegible] ***protein*** [illegible] ***protein*** interaction between the p85 subunit of PI 3-kinase, known to bind many proteins. Using the yeast ***two*** - ***hybrid*** system, in this study, we have identified a novel cellular protein that interacts with the p85 SH3 domain. We have also found that the SH3 domain of p85 associates with a serine/threonine-specific protein phosphatase activity in anti-SH3 immunoprecipitates. Using the phosphatase ***inhibitor*** okadaic acid and Western blotting, the phosphatase was identified as protein phosphatase 2A (PP2A). Mutation of a single amino acid. . .
CT [illegible]
[illegible]
[illegible]

*leukemia associated protein
*phosphoprotein phosphatase 2a
unclassified drug

L4 ANSWER 5 OF 38 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Molecular and Cellular Biology, [illegible]
Entry:
[illegible]

AB . . . pt the lysis by the Int proteasome. In an attempt to identify
[illegible] the I.kappa.B.alpha. inhibitory activity, we undertook a
yeast ***two*** - ***hybrid*** genetic screen, using the
amino-terminal end of I.kappa.B.alpha. as bait, and identified 17
independent interacting clones. Sequence analysis identified some . . .
DNA [illegible] as [illegible], a sequence with [illegible] a small, 2-kDa human [illegible]
the outer-arm dynein light-chain protein. In the ***two*** -
hybrid assay, Dlc-1 also interacted with full-length
I.kappa.B.alpha. protein but not with N-terminal-deletion-containing
versions of I.kappa.B.alpha.. I.kappa.B.alpha. interacted in vitro with.
. .
CT Medical Descriptors:
****protein protein interaction***
amino terminal sequence
animal cell
article
cell nucleus
cytoplasm
hela cell
human
human cell
immunofluorescence
kidney cell
microtubule
nonhuman
priority journal
*cytoskeleton protein
*cytoskeleton protein dlc 1
****inhibitor protein***
****inhibitor protein ikba***
alpha tubulin
dynein adenosine triphosphatase
glutathione transferase
hybrid protein
unclassified drug

L47 ANSWER 6 OF 38 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Proceedings of the National Academy of Sciences of the United States of
America, (1997) 94/23 (12401-12406).
Entry:
[illegible]

AB . . . [illegible] present in [illegible] . . . [illegible] . . . [illegible]
[illegible] ***two*** -
hybrid system, [illegible] [illegible], Dlc-1, Dlc-2,
[illegible] [illegible] [illegible], and Dlc-3, [illegible]
members. This . . . and different pro-apoptotic proteins. In mammalian
cells, overexpression of Bik induced apoptosis that was blocked by the
baculoviral-derived cysteine protease ***inhibitor*** p35. Cell
killing induced by Bik was also suppressed following coexpression with
Dlc-1 and [illegible] . . . with Bik-, [illegible]. . . .
CT Medical Descriptors:
. . . .

[illegible]
protein localization
protein protein interaction
rat
testis
uterus
*protein bcl-2: ED, endogenous compound
messenger rna: EC, endogenous compound

L47 ANSWER [illegible] OF [illegible] EMBASE COPYRIGHT [illegible] ELSEVIER SCI. B.V.
AU Molecular Endocrinology, (1997) 11:13 (1913-1920).
Refs: 43
ISSN: 0888-8809 CODEN: MOENEN
AB . . . that BAD, in addition to binding Bcl-XL and Bcl-2, may interact with proteins outside the Bcl-2 family. Using the yeast ***two*** - ***hybrid*** system to search for BAD-binding proteins in an ovarian tumor cDNA library, we identified multiple cDNA clones encoding different isoforms. . . . presumably resembles an underphosphorylated form of BAD, we used this mutant to screen for additional BAD-interacting proteins in the yeast ***two*** - ***hybrid*** system. 14-3-3, a nerve growth factor-induced neurite extension factor and member of the calcium-binding S-100 protein family, interacted strongly with. . . wild type BAD or its mutants increased apoptotic cell death, which was blocked by cotransfection with the baculovirus-derived cysteine protease ***inhibitor*** , P35. Cotransfection with 14-3-3 suppressed apoptosis induced by wild type or the S113A mutant BAD but not by the S137A. . .
CT Medical Descriptors:
*apoptosis
*protein targeting
animal cell
article
cell cycle
cell cell
controlled study
hormonal regulation
mammal cell
nonhuman
point mutation
priority journal
protein domain
protein family
protein polymorphism
protein protein interaction
signal transduction
*protein bcl-2
mutant protein
nerve growth factor
phosphatidylinositol kinase
protein kinase
[illegible]

L1 ANSWER [illegible] OF [illegible] EMBASE [illegible] ELSEVIER SCI. B.V.
AU Biochemical and Biophysical Research Communications, (1997) 235...
[illegible].
Refs: 22
ISSN: 0006-291X CODEN: BBRCA
AB [illegible]

priority journal
protein binding
protein protein interaction
*immunoglobulin enhancer binding protein
*protein
*rna polymerase ii
14 3 3 protein
interleukin 1beta
nitric oxide
nuclear protein
protein tyrosine kinase inhibitor
tumor necrosis factor
unclassified drug

L4 ANSWER 9 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Journal of Bacteriology, (1997) 179/17 (5551-5558).
Refs: 41
ISSN: 0021-9193 CODEN: JOBAAY
AB . . . with itself, GTP, and FtsA was examined by analyzing the sensitivity of FtsZ to proteolysis and by using the yeast ***two*** - ***hybrid*** system. The N-terminal conserved domain consisting of 320 amino acids bound GTP, and a central region of FtsZ, encompassing slightly. . . proteins from distantly related bacterial species. FtsZ120, which was truncated at the end of the conserved domain, was a potent ***inhibitor*** of division although it expressed normal GTPase activity and could polymerize. FtsZ was also found to interact directly with FtsA,. . .
CT Medical Descriptors:
protein protein interaction
amino terminal sequence
analytic method
article
carboxy terminal sequence
cross linking
cytoskeleton
enzyme activity
molecular interaction
nonhuman
priority journal
protein domain
site directed mutagenesis
temperature sensitivity

L4 ANSWER 10 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Cell, (1997) 90/2 (373-383).
Refs: 44
ISSN: 0092-8674 CODEN: CELLB5
AB . . . the transcription factor NF-kappa.B by tumor necrosis factor [illegible] NIK . . . NF-kappa.B activation, we have identified a novel protein, NIK-associated protein 1, which associates with NIK. . . . NIK-associated protein 1 inhibits NIK- and [illegible] ***inhibitory*** . IKK-, IL-1-, TRAF-, and NIK-induced NF-kappa.B activation. NAP1 associates with the NF-kappa.B inhibitor I.kappa.B-alpha., in mammalian cells. CONCLUSIONS: . . .
CT Medical Descriptors:
*tumor necrosis
animal cell

L47 ANSWER 11 OF 33 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
TI Yeast ***two*** - ***hybrid*** cloning of a novel zinc finger
protein that interacts with the multifunctional transcription factor YY1.
Nucleic Acids Research, [illegible]
Date: 19
[illegible] LIEN: MARMAL
AB . . . might mediate the functional stability of YY1 in muscle cells, we
screened an adult human muscle cDNA library using the yeast ***two***
hybrid cloning system. We report the isolation and
characterization of a novel protein termed YAF2 (YY1- associated factor 2)
that interacts. . . cleavage of YY1 by the calcium-activated protease
m-calpain. The isolation of YAF2 may help in understanding the mechanisms
through which ***inhibitors*** may exert transcription may be
differentially eliminated by proteolysis during myogenesis.
NT Medical Descriptors:
*acid resistance
*muscle development
*transcription regulation
amino acid sequence
amino terminal sequence
animal tissue
article
cell differentiation
controlled study
dna library
dna transfection
molecular cloning
muscle cell
myoblast
newborn
nonhuman
nucleotide sequence
priority journal
promoter region
protein degradation
protein protein interaction
rat
yeast
*transcription factor
*zinc finger protein
basic protein
calpain
lysine
messenger rna: EC, endogenous compound

L47 ANSWER 12 OF 33 EMBASE COPYRIGHT 2003 ELSEVIER SCI. B.V.
[illegible]
Date: 19
[illegible] LIEN: OTHER
AB A yeast ***two*** - ***hybrid*** [illegible] HBP1 a
transcriptional repressor interacting with the [illegible]
family. We show that HBP1. . . an activation domain. Two-fusion
experiments indicate that HBP1 contains a masked activation domain.
Deletion of two independent N- and C-terminal ***inhibitor*** domains
unmasks an activation domain which is 15-fold more active than the full
length protein. The released activation capacity is. . .
NT Medical Descriptors:
*acid resistance

protein protein interaction

ANSWER 14 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.

EMBO Journal., (1997) 16/6 (1413-1426).

Refs: 63

ISSN: 0261-4189 CODEN: EMJODG

AB We have isolated a human cDNA which encodes a novel I.kappa.B family member using a yeast ***two*** - ***hybrid*** screen for proteins able to interact with the p52 subunit of the transcription factor NF-.kappa.B. The protein is found in. . . give rise to a protein of 45 kDa, which exists as multiple phosphorylated isoforms in resting cells. Unlike the other ***inhibitors*** , it is found almost exclusively in complexes containing RelA and/or cRel. Upon activation, I.kappa.B-.epsilon. protein is degraded with slow kinetics. . .

CT Medical Descriptors:

human

kinetics

Refs: 4
ISSN: [illegible] CODEN: [illegible]
AB [illegible] which promotes mitosis by inhibiting Wee1 via direct
[illegible]. To understand better the function and regulation of Nim1,
the yeast ***two*** - ***hybrid*** system was used to identify
S.pombe cDNA clones encoding proteins that interact with Nim1. Sixteen of
the 17 cDNA clones. . .
CT Medical Descriptors:
amino terminal sequence
article
cell cycle
controlled study
enzyme activation
enzyme inhibition
mitosis
nonhuman
phenotype
priority journal
protein phosphorylation
protein protein interaction
schizosaccharomyces pombe
*antimitotic agent: EC, endogenous compound
complementary dna
cyclin dependent kinase: EC, endogenous compound
leucine zipper protein
protein serine threonine kinase: EC,. . .

L47 ANSWER 16 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI Inactivation of the cdk ***inhibitor*** p27(KIP1) by the human
papillomavirus type 16 E7 oncoprotein.
SO Oncogene, (1996) 13/11 (2323-2330).
Refs: 41
ISSN: 0950-9232 CODEN: ONCNES
AB . . . loss of cell adhesion, two experimental conditions in which cell
cycle progression is accompanied by elevated levels of the cdk
inhibitor p27(KIP1). We show here that E7 can antagonize the
ability of p27(KIP1) to block cyclin E-associated kinase in vitro and. .
. association requires the C-terminal part of E7. The interaction between
p27(KIP1) and E7 can also be demonstrated in a yeast ***two***
hybrid system. The data suggest that the ability of E7 to override
certain forms of G0/G1 arrest is mediated in part by binding to and
subsequent inactivation of the cdk ***inhibitor*** p27(KIP1).
CT Medical Descriptors:
****protein protein interaction***
*transcription regulation
*virus oncogene
*wart virus
animal cell
article
carboxy terminal sequence
[illegible]
[illegible]
[illegible]
mitosis inhibition
nonhuman
priority journal
[illegible]
protein
[illegible]

conserved region of p21 [redacted] acids 46-[redacted], which is homologous to similar regions in the related Cdk [redacted] ***inhibitors*** p27 and p57, can bind to Cdk2, and that this region is essential for kinase inhibition. However, the site's [redacted] molecules with various N-terminal and C-terminal [redacted] and tested each for their ability to bind [redacted] p21 by the yeast ****two*** - ***hybrid*** and [redacted] assays. None of the deletion mutants tested bound to p21 by either assay. We next tested whether p21 could bind to Cdk2, a component of the cyclin-activating kinase complex. By both the glutathione-binding and yeast ****two*** - ***hybrid*** assays, p21 failed to bind to this protein, consistent with previous reports. However, hybrid molecules containing the amino-terminal half [redacted]. Furthermore, the yeast Cdk2-p21 protein, which is identical with Cdk2, failed to bind to p21 by both the yeast ****two*** - ***hybrid*** and double-labeling assays. Cdk2/Cdc2 hybrids but not Cdc2/Cdk2 hybrids could bind to p21. These results suggest that the amino-terminal half [redacted].

CT Medical Descriptors:
*cancer
antineoplastic activity
article
cell cycle g1 phase
drug effect
enzyme activity
human
nonhuman
priority journal
protein protein interaction
transcription regulation
****cyclin dependent kinase inhibitor: ED, pharmacology***
*protein p21
cyclin dependent kinase

L47 ANSWER 18 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI RhoGDI-3 is a new GDP dissociation ***inhibitor*** (GDI): Identification of a non-cytosolic GDI protein interacting with the small GTP-binding proteins RhoB and RhoG.
SO Journal of Biological Chemistry, [1996] 271/48 (30366-30374).
ISSN: 0021-9258 CODEN: JBCHA3
AB [redacted] endogenous RhoB protein is regulated during the cell cycle, contrasting with the permanent RhoA protein expression (1). Using the yeast ***two*** - ***hybrid*** system to characterize proteins interacting with RhoB, we identified a new mouse Rho GDP dissociation ***inhibitor*** , referenced as RhoGDI-3. The NH2-terminal a helix of RhoGDI-3 is strongly amphipatic and differs thus from that found in previously [redacted] acting on Rab or Rho, RhoGDI-3 is associated to a Triton X-[redacted]- insoluble membranous or cytoskeletal subcellular fraction. In the ****two*** - ***hybrid*** system, RhoGDI-3 interacts [redacted]
CT [redacted]

[illegible] system has [illegible]
genome-wide mapping of ***protein*** - ***protein***
interactions, and the identification of peptide ***inhibitors***
of protein interactions. In addition, immunophilins and their chemical
ligands are providing useful reagents for [illegible]
protein - ***protein*** ***interactions*** in vivo to
dissect intracellular signaling pathways.
CT Medical Descriptors:
protein protein interaction
biochemistry
dimerization
gene mapping
[illegible]
[illegible]
nonhuman
priority journal
protein domain
short survey
signal transduction
dna binding protein
immunophilin
peptide

L4 ANSWER 20 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
SO Molecular and Cellular Biology, [illegible]
ISSN: [illegible] CODEN: MCEBD4
AB The E1B 19-kilodalton protein (19K protein) is a potent apoptosis
inhibitor and the adenovirus homolog of Bcl-2 (E. White, Genes
Dev. 10:1-15, 1996). To obtain a better understanding of the biochemical
. . which interact with E1B 19K and Bcl-2 and promote apoptosis. Like
Bax and Bak, Nbk was cloned from a yeast ***two*** - ***hybrid***
screen for proteins that interact with E1B 19K. Nbk contained BH3 but not
BH1 or BH2. It also interacted with. . . apoptosis. Nbk may therefore
represent a novel death regulator which contains only a BH3 that interacts
with and antagonizes apoptosis ***inhibitors*** such as the E1B 19K
protein.
CT Medical Descriptors:
*apoptosis
protein protein interaction
animal cell
article
molecular cloning
nonhuman
priority journal
protein family
protein induction
protein localization
[illegible]
[illegible]
[illegible]
[illegible]
[illegible]

L4 ANSWER 21 OF 33 EMBASE COPYRIGHT [illegible] ELSEVIER SCI. B.V.
TI [illegible] for a 'double-hybrid' assay for ***protein*** - ***protein***
interactions: localization of the CBF-binding domain to human
[illegible]
[illegible], [illegible], [illegible].
[illegible]; [illegible], [illegible].

[illegible]
[illegible]
human
molecular cloning
nonhuman
plasmid
priority journal
promoter region
protein binding
[illegible]
[illegible]
[illegible]

L47 ANSWER 22 OF 33 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
TI Interaction between FtsZ and ***inhibitors*** of cell division.
SO Journal of Bacteriology, (1996) [illegible].
ISSN: [illegible] CODEN: JOBAAY
AB The interaction between ***inhibitors*** of cell division and FtsZ were assessed by using the yeast ***two*** - ***hybrid*** system. An interaction was observed between FtsZ and SulA, a component of the SOS response, and the interacting regions were. . .
CT Medical Descriptors:
*cell division
article
dna hybridization
escherichia coli
gene mutation
nonhuman
priority journal
protein binding
protein domain
protein protein interaction
yeast

L47 ANSWER 23 OF 33 EMBASE COPYRIGHT 2001 ELSEVIER SCI. B.V.
SO Science, (1996) 272/5265 (1179-1182).
ISSN: 0036-8075 CODEN: SCIEAS
AB . . . kinase (MAPKKK) family, TAK1, was previously identified as a mediator in the signaling pathway of IGF-.beta. superfamily members. The yeast ***two*** - ***hybrid*** system has now revealed two human proteins, termed TAB1 and TAB2 (for TAK1 binding protein), that interact with TAK1. TAB1 and TAK1 were co-immunoprecipilated from mammalian cells. Overproduction of TAB1 enhanced activity of the plasminogen activator ***inhibitor*** 1 gene promoter, which is regulated by, TGF-.beta., and increased the kinase activity of TAK1. TAB1 may function as an. . .
CT Medical Descriptors:
*enzyme activation
*protein isolation
*signal transduction
article
[illegible]
human
[illegible]
nonhuman
priority journal
promoter region
protein binding
protein protein interaction
[illegible]
[illegible]

[illegible] the ability of [illegible] to [illegible] virus [illegible] of virus
-be., [illegible] [illegible] -type p[illegible], the viral I.kappa.B-.alpha. pr[illegible],
contributes to v-Rel-mediated oncogenesis. The yeast ***two***
hybrid system was utilized to dissect Rel:I.kappa.B-.alpha.
[illegible] [illegible] [illegible] [illegible] [illegible] [illegible]
[illegible].
CT Medical Descriptors:
*dna binding
*protein localization
amin[illegible] [illegible] sequence
article
cytoplasm
human
priority journal
protein domain
protein protein interaction
transactivation

L4 ANSWER 2 OF 33 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI A20, an ***inhibitor*** of cell death, self-associates by its zinc
finger domain.
SO FEBS Letters, (1996) 384/1 [illegible].
ISSN: 0014-5793 CODEN: FEBLAL
AB . . . cells. The A20 protein belongs to a novel class of Cys2/Cys2 zinc
finger proteins, and has been characterized as an ***inhibitor*** of
both apoptotic and necrotic cell death. In order to clarify its molecular
mechanism of action, we used the yeast-based ***two*** - ***hybrid***
system to screen for A20-associated proteins. Here we report that A20 is
able to self-associate, and demonstrate that the latter. . .
CT Medical Descriptors:
*apoptosis
*cell death
*gene induction
*necrosis: ET, etiology
*protein aggregation
article
controlled study
dna library
gene expression
human
human cell
immunoblotting
molecular cloning
priority journal
protein domain
protein protein interaction
[illegible]
[illegible]
yeast
[illegible]
*zinc finger protein: ET, endogenous compound
hybrid protein: ET, exogenous compound
protein A20: ET, endogenous compound
[illegible]

L4 ANSWER [illegible] OF [illegible] EMBASE [illegible] ELSEVIER SCI. B.V.

amino terminal sequence
animal cell
article
cell death
[illegible]
human
[illegible]
priority journal
protein binding
  protein protein interaction
[illegible]
[illegible]
[illegible]

L4 ANSWER [illegible] OF [illegible] EMBASE COPYRIGHT (C) ELSEVIER SCI. B.V.
TI Identification of a nuclear-specific cyclophilin which interacts with the proteinase ***inhibitor*** eglin c.
SO Biochemical Journal, (1996) 314/1 (313-319).
ISSN: 0264-6021 CODEN: BIJOAK
AB We have identified a novel human cyclophilin (hCyP-60) which interacts with the proteinase ***inhibitor*** eglin c using the yeast ***two*** - ***hybrid*** system. A cDNA isolated from a Raji B lymphocyte library reveals a domain showing sequence similarity to known cyclophilins flanked. . .
IT Medical Descriptors:
  protein protein interaction
amino acid sequence
animal cell
article
b lymphocyte
cell nucleus
cell strain k 562
controlled study
human
human cell
immunoblotting
immunohistochemistry
kidney
nonhuman
northern blotting
pancreas
priority journal
protein binding
protein domain
protein localization
raji cell
tissue
[illegible]
[illegible]
[illegible]

L4 ANSWER [illegible] OF [illegible] EMBASE [illegible] ELSEVIER SCI. B.V.
[illegible]
[illegible]
AB . . . mammalian cells reveals that it is tightly associated with a [illegible]
  [illegible] [illegible]

cell growth
cell population
controlled study
dna damage
dna replication
enzyme linked immunosorbent assay
human
human tissue
immunoprecipitation
mammal cell
mouse
nonhuman
priority. . .

L47 ANSWER 39 OF 55 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.
TI Interactions among members of the Bcl-2 protein family analyzed with a yeast ***two*** - ***hybrid*** system.
SO Proceedings of the National Academy of Sciences of the United States of America, (1994) 91/20 (9238-9242).
ISSN: 0027-8424 CODEN: PNASA6
AB . . . with itself and other members of the Bcl-2 family, including Bcl-X-L, Bcl-X-S, Mcl-1, and Bax, were explored with a yeast ***two*** - ***hybrid*** system. Fusion proteins were created by linking Bcl-2 family proteins to a LexA DNA-binding domain or a B42 trans-activation domain. ***Protein*** - ***protein*** ***interactions*** were examined by expression of these fusion proteins in Saccharomyces cerevisiae having a lacZ (.beta.-galactosidase) gene under control of a. . . operator. This approach gave evidence for Bcl-2 protein homodimerization. Bcl-2 also interacted with Bcl-X-L and Mcl-1 and with the dominant ***inhibitors*** Bax and Bcl-X-S. Bcl-X-L displayed the same pattern of combinatorial interactions with Bcl-2 family proteins as Bcl-2. Use of. . .
CT Medical Descriptors:
*protein family
protein protein interaction
article
deletion mutant
dimerization
dna sequence
enzyme assay
human
human cell
immunoblotting
molecular cloning
nonhuman
phenotype
plasmid
polymerase chain reaction
priority journal
saccharomyces cerevisiae
yeast cell
*hybrid protein
*fusion protein
beta galactosidase
cell extract
complementary dna
rna directed dna polymerase

L47 ANSWER 40 OF 55 EMBASE COPYRIGHT 2000 ELSEVIER SCI. B.V.

article
cell cycle g1 phase
cell cycle s phase
cell division
cell proliferation
cell structure
enzyme activation
enzyme activity
hit site
mutation
protein protein interaction
saccharomyces cerevisiae
temperature sensitive mutant
yeast
protein kinase: EC, endogenous compound

L47 ANSWER 31 OF 33 CAPLUS COPYRIGHT 2000 ACS
TI Identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6057101	A	20000502	US 1997-874825	19970613
US 6057098	A	20000502	US 1996-663824	19960614
CA 2257958	AA	19971218	CA 1997-2257958	19970613 <--

AB Methods are described for detecting ***protein*** - ***protein*** ***interactions*** , among two populations of proteins, each having a complexity of at least 1,000. For example, proteins are fused either to. . . and carrying one type each of the fusion proteins are mated together. Productive interactions between the two halves due to ***protein*** - ***protein*** ***interactions*** lead to the reconstitution of the transcriptional activator, which in turn leads to the activation of a reporter gene contg.. . . carried out for two or more populations of proteins. The differences in the genes encoding the proteins involved in the ***protein*** - ***protein*** ***interactions*** are characterized, thus leading to the identification of specific ***protein*** - ***protein*** ***interactions*** , and the genes encoding the interacting proteins, relevant to a particular tissue, stage or disease. Furthermore, ***inhibitors*** that interfere with these ***protein*** - ***protein*** ***interactions*** are identified by their ability to inactivate a reporter gene. The screening for such ***inhibitors*** can be in a multiplexed format where a set of ***inhibitors*** will be screened against a library of interactors. Further, information-processing methods and systems are described. These methods and systems provide for
[illegible]
yeast protein interaction ***inhibitor*** ; human disease specific protein interaction
IT [illegible]
RL: BSU (Biological study, unclassified); BUU (Biological use, unspecified); BIOL (Biological study); USES (Uses)
[illegible]

inhibitors
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
([illegible]; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***
IT Protein motifs
(DNA binding domain, fusion proteins contg.; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Proteins, specific or class
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(DNA-binding; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Proteins, specific or class
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(FKBP-12 (FK 506-binding protein, 12,000-mol.-wt.), assay of interaction between R4 and FKBP12; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GAL4, DNA binding domain of; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GCN4, DNA binding domain of; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GFP; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(GUS, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
([illegible], reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)
IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
([illegible], reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***

(VP16-LEA; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(VP16, of herpes simplex virus; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Gene, microbial
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(cat, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Computer application
(computer-implemented data store; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene ARD1; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene Ace1N; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Vascular endothelial growth factor receptors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(gene KDR, interaction with VEGF or; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT [illegible]
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
[illegible]
protein - ***protein*** ***interactions*** and identification of ***inhibitors***

IT Transcription factors
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
[illegible]
protein - ***protein*** ***interactions*** and

interaction assay carried out in; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Biological methods

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(interaction with KDR of; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Enzyme, microbial

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(lacZ, reporter gene; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Animal cell

(mammalian; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Bacteria (Escherichia)

Saccharomyces cerevisiae

Yeast

(assay carried out in; identification and comparison of ***protein*** - ***protein*** ***interaction*** assay carried out in; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Genetic methods

(quant. expression anal. (QEA); identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT cDNA library

(screening of; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Protein motifs

(transcriptional regulatory domain, fusion proteins contg.; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT Genetic methods

(***two*** - ***hybrid*** system; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT 127464-60-2, Vascular endothelial growth factor

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(interaction with KDR of; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT 61-68-5, 1H-1,2,4-Triazol-3-amine 61-90-5, L-Leucine, biological studies [illegible]

RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

(identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT [illegible] 4: PN: WO9701349 PAGE: 23 unclaimed DNA 127461-10-5 [illegible] DNA [illegible]

[illegible] DNA [illegible] unclaimed DNA
[illegible] 266333-91-9 266333-92-0 266333-93-1 266333-94-2
266333-95-3 266333-96-4 266333-97-5 266333-98-6 266333-99-7
[illegible]
266334-50-3 266334-51-4 [illegible] [illegible] [illegible]
[illegible] 266334-56-9 266334-57-0 266334-58-1 266334-59-2
[illegible] 266334-61-6 266334-62-7 [illegible] 266334-64-9
[illegible] 266334-66-1 266334-67-2 266334-68-3 266334-69-4
266334-70-7

RL: PRP (Properties)
(unclaimed nucleotide sequence; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

IT 95088-49-6
RL: PRP (Properties)
(unclaimed sequence; identification and comparison of ***protein*** - ***protein*** ***interactions*** and identification of ***inhibitors***)

L4 ANSWER 32 OF 33 CAPLUS COPYRIGHT 2000 ACS

TI ***Two*** - ***hybrid*** screening and the cell cycle

SO Yeast Two-Hybrid Syst. (***1997***), 183-196. Editor(s): Bartel, Paul L.; Fields, Stanley. Publisher: Oxford University Press, New York, N. Y. CODEN: 65YDA2

AB A review with 61 refs. The ***two*** - ***hybrid*** screen has been most often successful in the identification of stable, ***protein*** - ***protein*** ***interactions*** . Perhaps, because such interactions are prevalent among components of cell cycle control, cell cycle regulatory proteins have proven amenable to the ***two*** - ***hybrid*** approach. Here, the authors discusses three aspects of cell cycle control in which the ***two*** - ***hybrid*** technique has been of particular importance. These are the regulation of the G1/S transition by phosphorylation of pRb, global control of cell cycle progression by the p21/p27 family of cyclin-dependent kinase (CDK) ***inhibitors*** and the role of CDK-activating kinase (CAK) and KAP in the metab. of threonine ~160 phosphorylation.

ST ***two*** ***hybrid*** screen cell cycle review

IT Interphase (cell cycle)
[illegible]

IT [illegible]
RL: [illegible]
[illegible]
p21, cyclin-dependent kinase ***inhibitors*** ; [illegible]
- ***hybrid*** screening in analyzing ***protein*** -
protein ***interactions*** involved in cell cycle)

IT [illegible]
RL: [illegible]
[illegible]

[illegible]

IT [illegible]
two - ***hybrid*** [illegible] ***two*** -
hybrid screening in analysing ***protein*** ***protein***
interactions involved in cell cycle

[illegible]
RL: BAC (Biological activity or effector, except adverse); BIOL
(Biological study)
(KAP; role of ***two*** - ***hybrid*** screening in analysing
protein - ***protein*** ***interactions*** involved in
cell cycle)

IT [illegible], L-Threonine, biological studies
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(phosphorylation; role of ***two*** - ***hybrid*** screening in
analysing ***protein*** - ***protein*** ***interactions***
involved in cell cycle)

IT 143443-83-1, Cyclin-dependent kinase-activating kinase
RL: BAC (Biological activity or effector, except adverse); BIOL
(Biological study)
role of ***two*** - ***hybrid*** screening in analysing
protein - ***protein*** ***interactions*** involved in
cell cycle)

IT 150405-21-5, Cyclin-dependent kinase
RL: BAC (Biological activity or effector, except adverse); BPR (Biological
process); BIOL (Biological study); PROC (Process)
(role of ***two*** - ***hybrid*** screening in analysing
protein - ***protein*** ***interactions*** involved in
cell cycle)

L47 ANSWER 33 OF 33 BIOSIS COPYRIGHT 2010 BIOSIS
SO Biochemical and Biophysical Research Communications, (1995) Vol. 215, No. 2, pp. 781-790.
ISSN: 0006-291X.
AB. . . by its autoinhibitory domain (AID) and by the calcium-binding proteins calcineurin B (CnB) and calmodulin. We have used the yeast ***two*** - ***hybrid*** system to show that AID, CnB and calmodulin can only bind to a truncated catalytic subunit of yeast calcineurin (i.e., . . . the mechanism by which drug-receptor complexes could modulate calcineurin activity but also unveil the possibility of identifying novel immunophilin-independent calcineurin ***inhibitors*** which may disturb the association of CnA1-DELTA to AID.
IT Miscellaneous Descriptors
CALCINEURIN B; CALMODULIN; DRUG-RECEPTOR COMPLEX; PHARMACODYNAMICS; ***PROTEIN*** - ***PROTEIN*** ***INTERACTION*** ; T-CELL ACTIVATION

=> log h

[illegible]